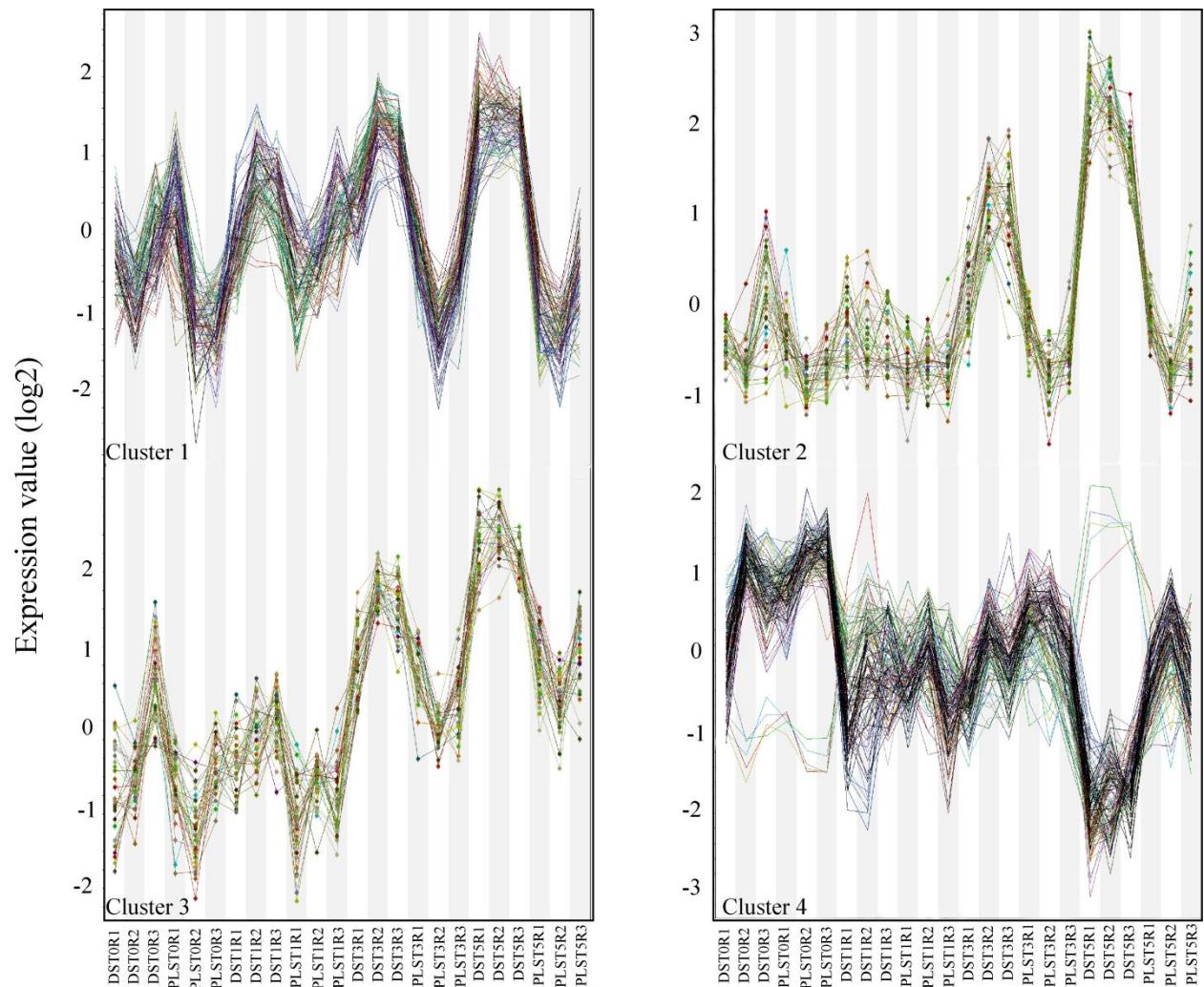
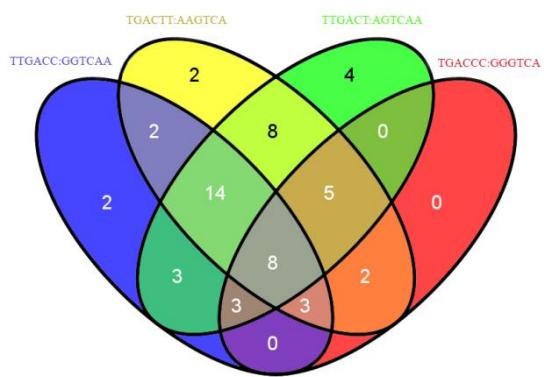


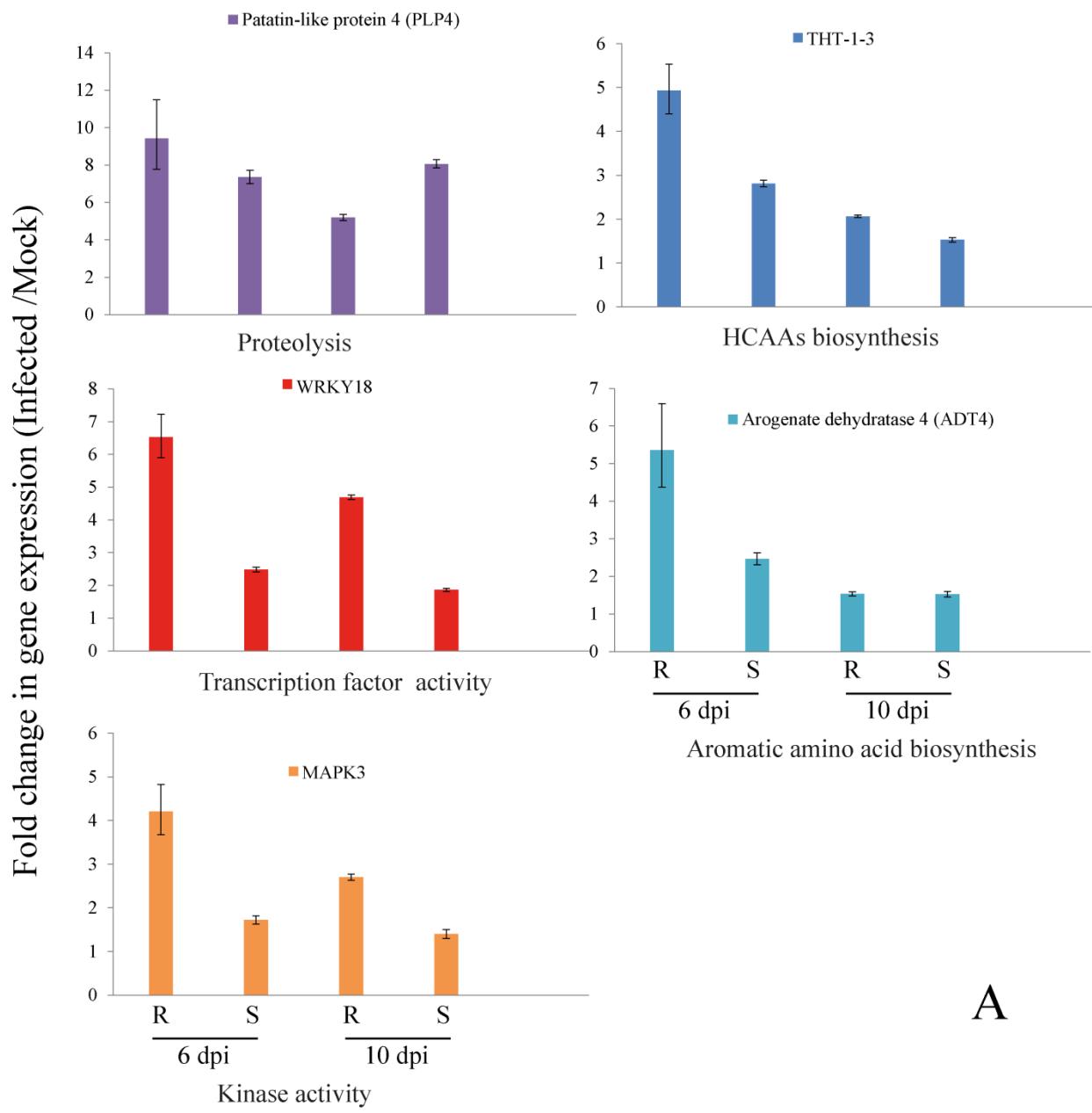
Supplemental Figures

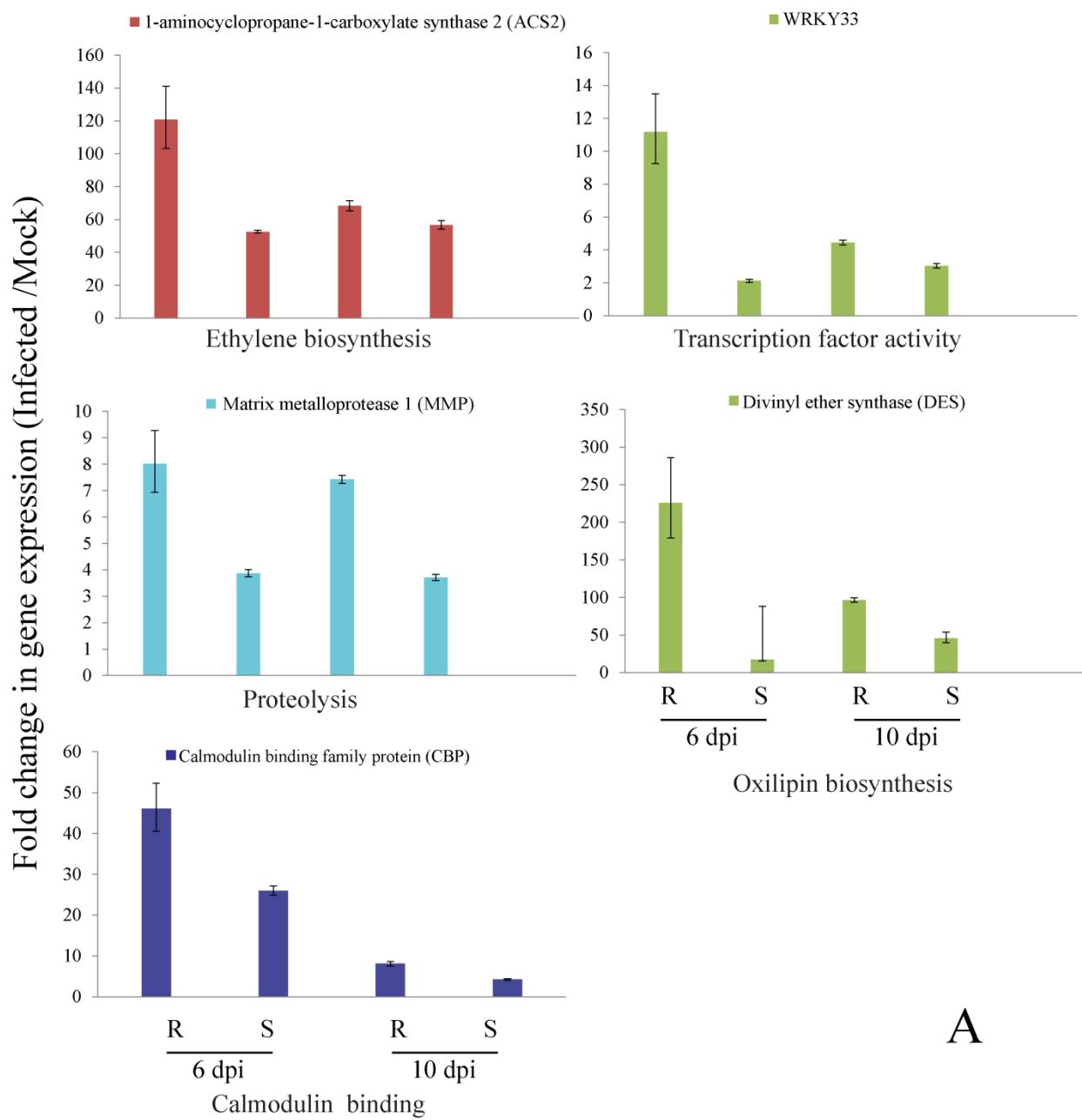


Supplemental Figure S1. Expression profiles of the different gene clusters identified in the co-expression network analysis of differentially regulated genes during mounting of the HR in the dying seedlings (DS), as shown in Fig. 4A. The log₂ expression value for every gene in the individual clusters was normalized for offset with the cluster average value and scaled by the standard deviation of the cluster. DS, dying seedlings; PLS, parental lines; T, time after the temperature shift (0 hr, 1 hr, 3 hr or 5hr); R, replicate number (1, 2 or 3). Each time point is represented by three independent biological replicates (see Materials and Methods for details).

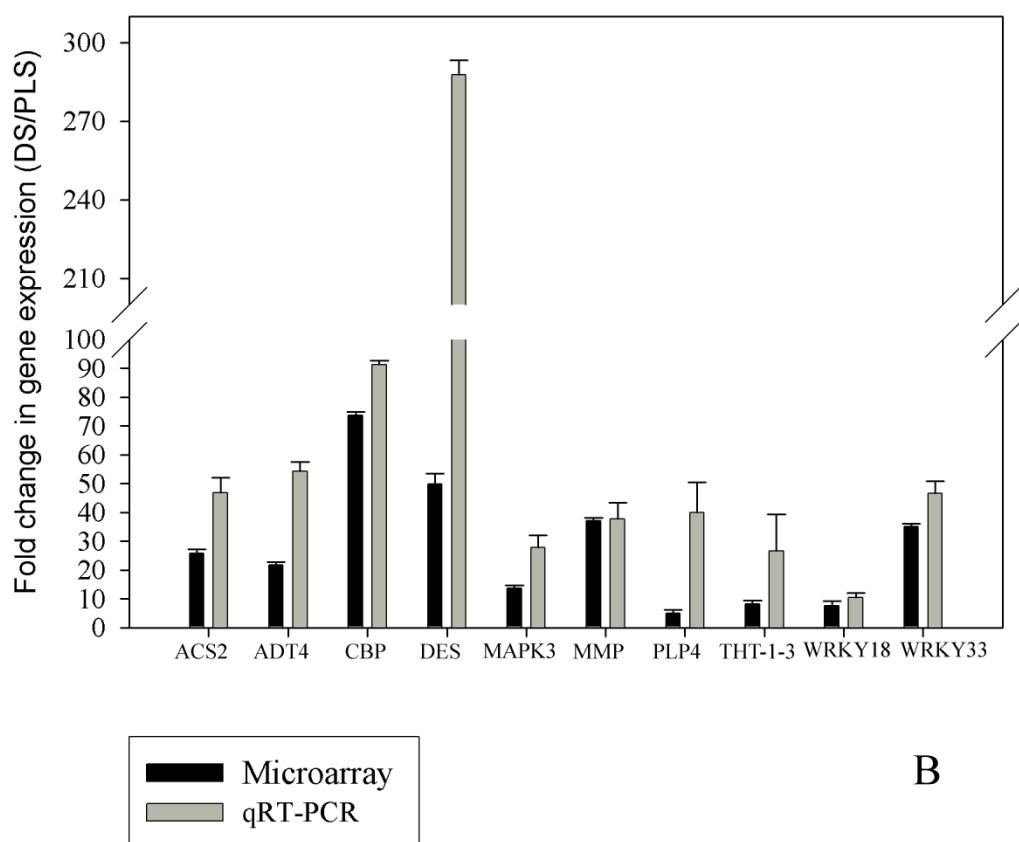


Supplemental Figure S2. Venn diagram showing the number and distribution of genes containing the sequence TTTGAC, interrogated for the presence of either a C or a T, following the core sequence TGAC. Note that from the 60 genes that were analyzed (see Supplementary Table S4), 56 contain the TGACC/T W box consensus core motif.

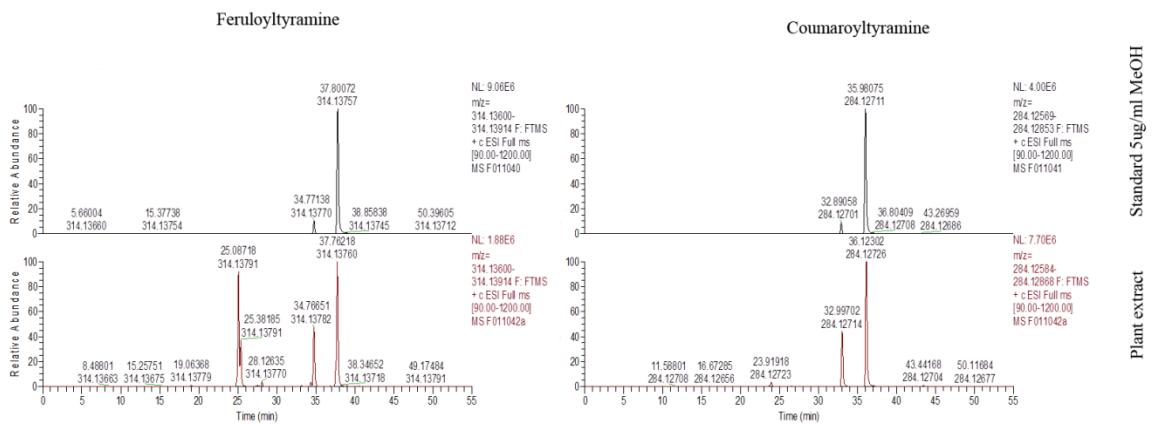




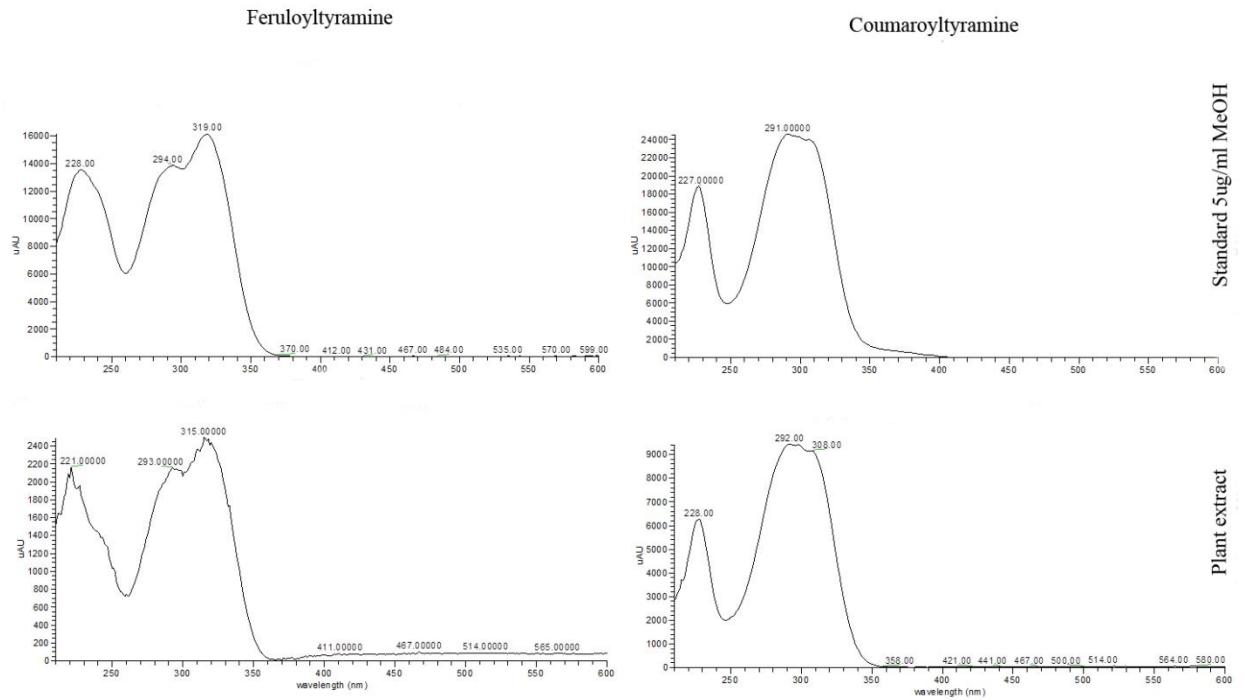
A



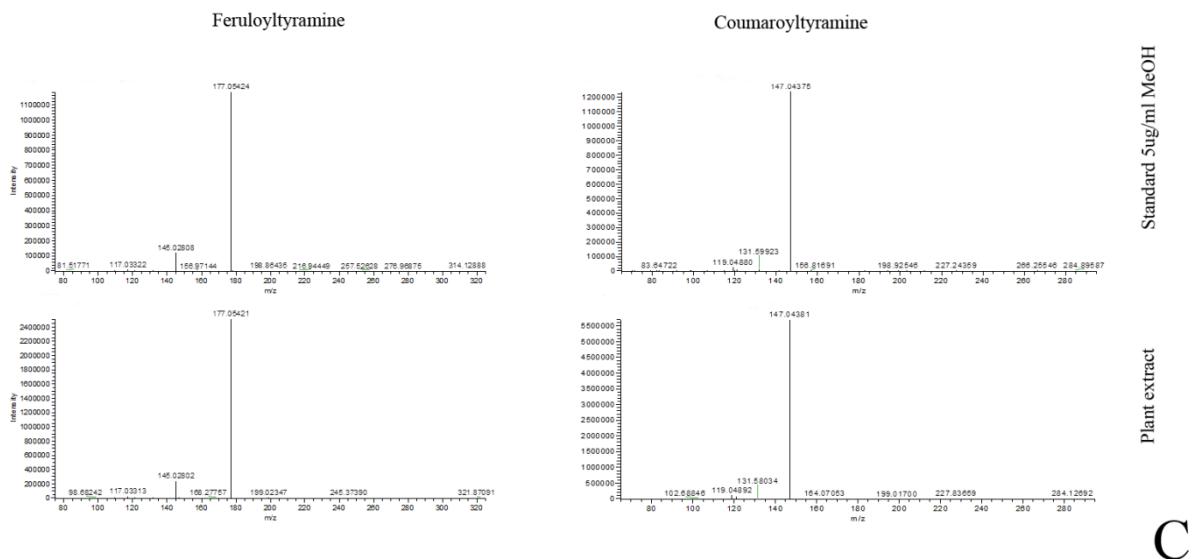
Supplemental Figure S3. Quantitative RT-PCR analysis of the expression of genes, selected from the co-expression network analysis of the dying seedlings (DS), in leaves of *C. fulvum*-inoculated tomato. A, Parental lines (PLS) used to generate the dying seedlings (MM-Cf0: Cf-4, resistant (R) and MM-Cf0: Avr4, susceptible (S)), were inoculated with a strain of *C. fulvum* secreting Avr4. Gene expression levels, in fold change relative to mock-treated plants, were determined at 6 and 10 days after inoculation (dpi). B, Comparison of the relative expression levels of the selected genes, as determined by the microarray analysis and by qRT-PCR, in the DS compared to the PLS, at t = 3 hr after the temperature shift that triggers the HR in the DS.



A



B



Supplemental Figure S4. Confirmation of the identity of trans-feruloyltyramine (FT) and trans-coumaroyltyramine (CT) present in total extracts of dying seedlings obtained at 5 hr after the temperature shift, using synthesized trans-FT and trans-CT as standards. A, Chromatography of the trans-FT and trans-CT standards (upper graphs) and total extract (lower graphs). B, UV absorption spectra of the trans-FT and trans-CT standards (upper graphs) and total extract (lower graphs). C, MS/MS spectra of the trans-FT and trans-CT standards (upper graphs) and total extract (lower graphs). See Materials and Methods for details.

Supplemental Materials and Methods S1.

Reduction of the redundancy of GO: subcategories obtained from GeneTrail

The Gene x GO: subcategory matrix presented in Table 1 is an output from GeneTrail. When a gene is reported to be involved in one of the listed GO: subcategories it obtains a score of “1”, otherwise the score is “0”.

Table 1.

Example of a GO: subcategory x Gene matrix, an output from GeneTrail, representing genes reported to be involved in posttranslational protein modification (phosphorylation).

GO: subcategory	Significantly differentially regulated genes										
	ATMPK3	CPK32	AT1G25390	CDPK19	CPK28	APK1B	AT3G09830	ATSIK	AT2G05940	AT3G57700	AT4G17660
protein tyrosine kinase activity (GO:0004713)	0	0	0	0	1	1	0	1	0	0	1
protein modification process (GO:0006464)¹	1	1	1	1	1	1	1	1	1	1	1
post-translational protein modification (GO:0043687)	1	1	1	1	1	1	1	1	1	1	1
macromolecule modification (GO:0043412)	1	1	1	1	1	1	1	1	1	1	1
phosphorus metabolic process (GO:0006793)	1	1	1	1	1	1	1	1	1	1	1
phosphate metabolic process (GO:0006796)	1	1	1	1	1	1	1	1	1	1	1
protein amino acid phosphorylation	1	1	1	1	1	1	1	1	1	1	1
phosphorylation (GO:0016310)	1	1	1	1	1	1	1	1	1	1	1
protein serine/threonine kinase activity (GO:0004674)	1	1	0	1	1	1	0	0	1	1	1
kinase activity (GO:0016301)	1	1	1	1	1	1	1	1	1	1	1
transferase activity, transferring phosphorus-containing groups	1	1	1	1	1	1	1	1	1	1	1
protein kinase activity (GO:0004672)	1	1	0	1	1	1	1	1	1	1	1
phosphotransferase activity, alcohol group as acceptor (GO:0016773)	1	1	0	1	1	1	1	1	1	1	1

¹GO: subcategories that share a complete set of genes are indicated in bold. See text below.

Two GO: subcategories “i” and “j” may be compared on the characteristic presence of a differentially regulated gene “k” and are assigned a score S_{ijk} . This score is “0” when the two subcategories are considered to be different, as similar genes are not present. The score increases to “1” when more genes common to both functional groups are present. Thus, S_{ijk} is defined by a range between “0” and “1”, in which a value of “1” means that two or more of the functional categories share the same genes (see GO: subcategories that are indicated in bold). This is represented by the red blocks along the diagonal axis in Fig. 1. A value of “0” indicates that the functional categories do not share any gene, which is represented by blue in

Fig. 1. Based on this principle, the similarity between the different GO: subcategories was computed in the program “R” (Fig. 1). As the matrix is a mirrored image of itself, only half of the rectangle is shown (see also Fig. 3 of the manuscript). Categories that represent similar functional processes were given one description. For example, all GO: subcategories merging in the red triangle in the black boxed region in Fig. 1 represent protein modification (phosphorylation).

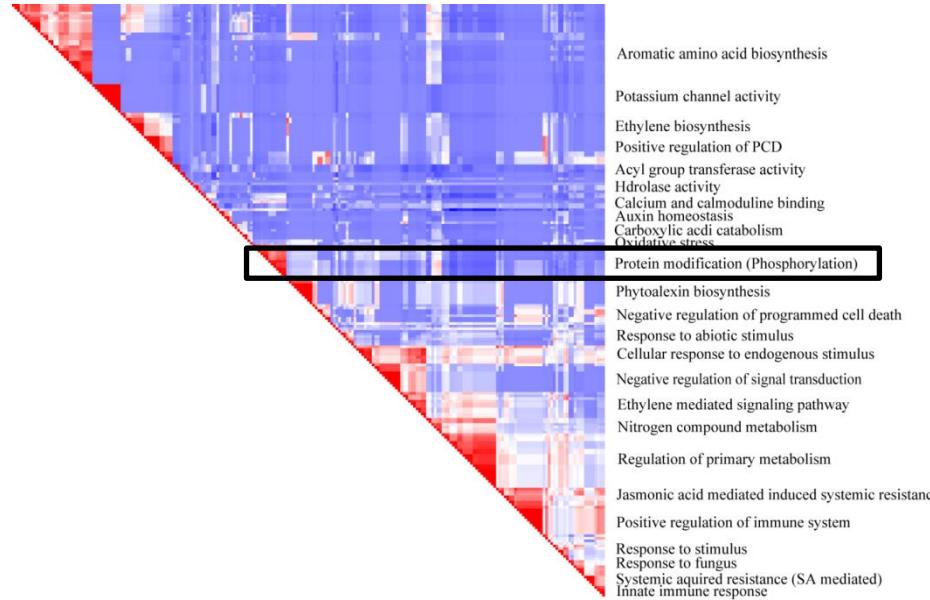


Figure 1. GO: sub-category similarity matrix, resulting from the GeneTrail GO: subcategory x Gene matrix. The red clusters along the diagonal axis represent highly similar GO: sub-categories.

Supplemental Table S1. Expression profiles of genes encoding heat shock proteins in the dying seedlings (DS) compared to the parental lines (PLS). Expression levels are given as fold change (FC) in gene expression in the DS as compared to the PLS at 0, 1, 3 and 5 hr after the temperature shift that induces the HR in the DS.

Probe set ID	Best Arabidopsis hit	Best Arabidopsis hit description	Fold change			
			0 hr	1 hr	3 hr	5 hr
Les.3160.3.S1_at	AT3G12580.1	HSP70 (heat shock protein 70); AT binding	1	1	1	3
Les.4819.1.S1_at	AT5G02500.1	HSC70-1 (heat shock cognate protein 70-1); AT binding	1	-1	7	22
Les.3160.2.S1_at	AT3G12580.1	HSP70 (heat shock protein 70); AT binding	1	1	-1	3
Les.3160.1.S1_at	AT1G56410.1	ERD2 (early responsive to dehydration 2); AT binding	1	-1	-1	2
Les.3657.1.S1_at	AT3G12580.1	HSP70 (heat shock protein 70); AT binding	1	1	1	10
Les.14662	At3g14200.1	DNAJ heat shock N-terminal domain-containing protein	1	1	-1	6

Supplemental Table S2. Significantly over-represented GO: subcategories in the dying seedlings (DS), at 1 hr after the temperature shift.

Category	Subcategory	Expected	Observed	P-value (FDR) ¹
Kegg	Valine, leucine and isoleucine degradation	0.089	2	0.00960
Gene Ontology	Oxidoreductase activity, acting on the aldehyde- or oxo- group of donors, disulfide as acceptor	0.025	2	0.02676
Gene Ontology	Response to chemical stimulus	3.713	12	0.02676
Gene Ontology	Secondary metabolic process	0.765	5	0.04839
Gene Ontology	Response to stimulus	7.030	16	0.04839

¹False discovery rate.

Supplemental Table S3. Description of the genes that cluster in groups of strongly associated genes that were identified by co-expression network analysis using Cytoscape, their relative fold change (FC) in expression in the dying seedlings compared to the parental lines at t = 0, 1, 3 and 5 hr, and output of the computation of the GO: enrichment analysis for each cluster.

Cluster 1 genes.

Probe set ID	ATH best hit	Bet hit description	FC 0 hr	FC 1 hr	FC 3 hr	FC 5 hr	Gene bank best hit description	Category
Les.3505.1.S1_at	AT2G15080	AtRLP19 (Receptor Like Protein 19); kinase/ protein binding	2.45	2.20	19.27	17.65	verticillium wilt disease resistance protein [Lycopersicon esculentum]	RLK
Les.2137.1.S1_at	AT2G15080	AtRLP19 (Receptor Like Protein 19); kinase/ protein binding	1.48	2.86	5.83	13.03	EIX receptor 1 [Lycopersicon esculentum]	
Les.4870.1.S1_at	AT4G20780	calcium-binding protein, putative	1.02	1.38	2.37	4.19	RecName: Full=Calcium-binding protein CAST	Calcium/Calmodulin signaling network
LesAffx.63947.2.S1_at	AT3G57530	CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium-dependent protein kinase C/calmodulin-dependent protein kinase/ kinase/ protein binding	1.03	1.15	3.70	4.20	calcium-dependent protein kinase 4 [Capsicum annuum]	
LesAffx.30900.1.S1_at	AT5G19450	CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); ATP binding / calcium ion binding /calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	1.03	1.31	2.97	4.13	calcium-dependent protein kinase 4 [Capsicum annuum]	
Les.5197.1.S1_at	AT2G18750	calmodulin-binding protein	-1.09	1.36	2.88	3.62	calmodulin binding protein [Zea mays]	
LesAffx.3635.2.A1_at	AT5G57010	calmodulin-binding family protein	2.43	4.09	31.74	69.36	calmodulin-binding protein [Beta vulgaris]	
LesAffx.69808.1.S1_at	AT2G26190	calmodulin-binding family protein	-1.05	3.08	73.60	268.67	calmodulin binding protein, putative [Ricinus communis]	
LesAffx.66814.1.S1_at	AT1G73805	calmodulin binding	1.19	-1.18	5.15	7.49	calmodulin binding protein, putative [Ricinus communis]	
LesAffx.3635.1.S1_at	AT4G33050	EDA39 (embryo sac development arrest 39); calmodulin binding	1.75	1.92	50.24	137.09	calmodulin binding protein, putative [Ricinus communis]	
Les.4316.1.S1_at	AT3G45640	ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-	1.04	1.11	7.33	13.74	mitogen-activated protein kinase 3 [Lycopersicon esculentum]	MAPK

		ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase						
LesAffx.16424.1.S1_s_at	AT3G45640	ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase	-1.01	1.25	7.38	13.27	mitogen-activated protein kinase 3 [<i>Lycopersicon esculentum</i>]	
LesAffx.65273.1.S1_at	AT1G16670	protein kinase family protein	1.09	1.41	1.93	4.00	ATP binding protein, putative [<i>Ricinus communis</i>]	Protein kinases
Les.1806.1.S1_at	AT3G09830	protein kinase, putative	1.25	1.34	2.31	3.86	protein kinase, putative [<i>Arabidopsis thaliana</i>]	
Les.3502.1.S1_at	AT2G05940	protein kinase, putative	-1.59	-1.04	19.44	55.33	auxin-regulated dual specificity cytosolic kinase [<i>Lycopersicon esculentum</i>]	
LesAffx.10313.1.A1_at	AT2G17220	protein kinase, putative	1.55	2.31	4.74	7.93	serine/threonine-protein kinase cx32, putative [<i>Ricinus communis</i>]	
Les.5205.1.S1_at	AT2G31880	leucine-rich repeat transmembrane protein kinase, putative	1.20	1.24	2.13	3.14	receptor-like protein kinase [<i>Nicotiana tabacum</i>]	LRRs
LesAffx.71532.1.S1_at	AT1G33590	disease resistance protein-related / LRR protein-related	1.33	1.25	3.01	4.39	disease resistance protein/LRR protein-related protein [<i>Glycine max</i>]	
Les.3710.1.S1_at	AT1G13580	LAG13 (LAG1 LONGEVITY ASSURANCE HOMOLOG 3)	1.25	2.84	50.45	70.82	RecName: Full=Protein ASC1; AltName: Full=Alternaria stem canker resistance protein 1	
LesAffx.42451.1.S1_at	AT4G00330	CRCK2; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	2.44	1.99	3.67	18.74	ATP binding protein, putative [<i>Ricinus communis</i>]	
Les.1297.1.S1_at	AT3G21630	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase	1.38	1.19	2.31	5.03	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [<i>Arabidopsis thaliana</i>]	
LesAffx.37337.1.S1_at	AT1G65960	GAD2 (GLUTAMATE DECARBOXYLASE 2); calmodulin binding / glutamate decarboxylase	1.98	2.76	21.57	36.61	glutamate decarboxylase isozyme 3 [<i>Nicotiana tabacum</i>]	
Les.3526.1.S1_a_at	AT2G20900	diacylglycerol kinase, putative	1.38	1.56	1.97	6.46	diacylglycerol kinase [<i>Lycopersicon esculentum</i>]	Phospholipid signaling
LesAffx.64831.1.S1_at	AT3G26020	serine/threonine protein phosphatase 2A (PP2A)	1.41	1.35	1.92	3.80	protein phosphatase 2A regulatory subunit B' [<i>Zea mays</i>]	

		regulatory subunit B', putative						
Les.3262.2.S1_at	AT2G46500	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	-1.17	1.16	1.61	2.37	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana]	
Les.3262.3.S1_at	AT2G46500	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	-1.10	-1.01	1.67	2.20	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana]	
Les.3493.1.S1_at	AT2G42010	PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D	2.00	2.12	7.28	20.66	phospholipase PLDb1 [Lycopersicon esculentum]	
LesAffx.36712.1.S1_at	AT4G23810	WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	1.61	1.40	16.03	19.42	WRKY transcription factor-30 [Capsicum annuum]	WRKY-TFs
LesAffx.51257.1.S1_at	AT5G64810	WRKY51; transcription factor	2.40	3.34	16.84	27.34	putative WRKY transcription factor [Nicotiana tabacum]	
LesAffx.735.1.S1_at	AT2G38470	WRKY33; transcription factor	-1.17	1.92	34.99	53.09	WRKY-like transcription factor [Solanum peruvianum]	
Les.3964.1.S1_at	AT4G31550	WRKY11; calmodulin binding / transcription factor	2.50	1.61	7.88	13.74	PREDICTED: similar to DNA-binding protein [Vitis vinifera]	
LesAffx.33402.1.A1_at	AT1G02170	AMC1 (METACASPASE 1); cysteine-type endopeptidase	1.30	1.47	5.59	6.98	caspase, putative [Ricinus communis]	
LesAffx.63935.1.S1_at	AT1G24140	matrixin family protein	1.46	1.75	37.08	49.68	matrix metalloprotease 1 [Nicotiana tabacum]	Protein degradation and programmed cell death
Les.5240.1.S1_at	AT2G05920	subtilase family protein	1.49	1.57	2.73	5.05	subtilisin-like protease [Solanum lycopersicum]	
LesAffx.57572.1.S1_at	AT4G37060	PLP5 (PATATIN-LIKE PROTEIN 5); nutrient reservoir	2.76	1.37	15.52	33.85	patatin-like protein 3 [Nicotiana tabacum]	
Les.5884.1.S1_at	AT1G17860	trypsin and protease inhibitor family protein / Kunitz family protein	1.61	2.29	5.51	11.45	miraculin-like protein [Solanum brevidens]	
LesAffx.44417.1.S1_at	AT3G25070	RIN4 (RPM1 INTERACTING PROTEIN 4); protein binding	1.26	1.52	3.70	6.71	RPM1-interacting protein 4 [Arabidopsis thaliana]	
Les.5077.1.S1_at	AT1G28380	NSL1 (necrotic spotted lesions 1)	1.35	1.56	2.01	4.70	NSL1 (necrotic spotted lesions 1) [Arabidopsis thaliana]	
Les.335.1.S1_at	AT5G47910	RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	1.24	1.50	4.91	5.97	whitefly-induced gp91-phox [Lycopersicon esculentum]	
LesAffx.20391.1.S1_at	AT1G23390	kelch repeat-containing F-box family protein	1.37	1.60	14.34	33.73	F-box/kelch protein [Vitis vinifera]	

LesAffx.30842.1.S1_at	AT2G27310	F-box family protein	-1.19	1.67	12.27	18.53	F-box family protein [Arabidopsis thaliana]	
LesAffx.30842.1.A1_at	AT2G27310	F-box family protein	-1.34	1.05	5.93	6.84	F-box family protein [Arabidopsis thaliana]	
LesAffx.71026.2.S1_at	AT5G62460	zinc finger (C3HC4-type RING finger) family protein	1.48	1.26	3.00	6.37	membrane associated ring finger 1,8, putative [Ricinus communis]	
LesAffx.71026.1.S1_at	AT3G47550	zinc finger (C3HC4-type RING finger) family protein	1.00	1.22	3.20	5.16	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	
Les.4671.1.S1_at	AT4G34040	zinc finger (C3HC4-type RING finger) family protein	-1.11	1.21	1.89	2.44	protein binding protein, putative [Ricinus communis]	
Les.4712.1.S1_at	AT1G49850	zinc finger (C3HC4-type RING finger) family protein	-1.30	1.73	6.87	8.70	RING-H2 finger protein [Glycine max]	
Les.5293.1.S1_at	AT2G26640	KCS11 (3-KETOACYL-COA SYNTHASE 11); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	1.11	1.28	5.55	8.14	beta-ketoacyl-CoA synthase [Helianthus annuus]	
Les.62.1.S1_at	AT4G35670	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	1.55	2.35	5.94	14.67	polygalacturonase [Lycopersicon esculentum]	Hydrolases
Les.3460.1.S1_at	AT3G52600	AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds	2.41	2.45	4.18	13.25	acid invertase [Solanum lycopersicum]	
LesAffx.10955.2.S1_at	AT1G08250	ADT6 (arogenate dehydratase 6); arogenate dehydratase/ prephenate dehydratase	1.88	1.65	17.40	41.82	putative arogenate dehydratase [Capsicum annuum]	Aromatic amino acid biosynthesis and transport
LesAffx.10955.1.S1_at	AT3G44720	ADT4 (arogenate dehydratase 4); arogenate dehydratase/ prephenate dehydratase	1.74	1.79	21.72	67.92	putative arogenate dehydratase [Capsicum annuum]	
Les.5555.1.S1_at	AT1G15710	prephenate dehydrogenase family protein	-1.18	1.29	3.32	5.06	prephenate dehydrogenase, putative [Ricinus communis]	
LesAffx.10955.3.S1_at	AT2G27820	PD1 (PREPHENATE DEHYDRATASE 1); arogenate dehydratase/ prephenate dehydratase	1.32	1.71	14.91	35.09	putative arogenate dehydratase [Capsicum annuum]	
Les.5279.1.S1_at	AT1G47670	amino acid transporter family protein	1.14	1.30	6.40	9.52	amino acid transporter, putative [Ricinus communis]	
LesAffx.71577.1.S1_a_at	AT2G19740	60S ribosomal protein L31 (RPL31A)	1.61	1.73	7.16	10.42	RecName: Full=60S ribosomal protein L31	
Les.4822.1.S1_at	AT2G39890	PROT1 (PROLINE TRANSPORTER 1); L-proline transmembrane	1.20	1.92	2.81	5.88	proline transporter 1 [Lycopersicon esculentum]	

		transporter/ amino acid transmembrane transporter						
Les.3686.1.S1_at	AT2G39030	GCN5-related N-acetyltransferase (GNAT) family protein	1.96	1.91	4.56	8.05	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT7-8 [<i>Lycopersicon esculentum</i>]	HCAAs biosynthesis
Les.4038.1.S1_at	AT2G39030	GCN5-related N-acetyltransferase (GNAT) family protein	1.22	1.88	8.28	26.38	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT1-3 [<i>Lycopersicon esculentum</i>]	
LesAffx.62617.1.S1_at	AT5G42830	transferase family protein	1.57	1.71	26.90	72.99	Anthranilate N-benzoyltransferase protein, putative [<i>Ricinus communis</i>]	
LesAffx.5435.1.S1_at	AT2G46960	CYP709B1; electron carrier/heme binding / iron ion binding / monooxygenase/oxygen binding	1.69	1.67	3.52	6.81	cytochrome P450 [Populus trichocarpa]	
Les.5485.1.S1_at	AT2G23810	TET8 (TETRASPAVIN8)	-1.09	1.02	2.46	2.91	TET8 (TETRASPAVIN8) [<i>Arabidopsis thaliana</i>]	
Les.4429.1.S1_at	AT5G47710	C2 domain-containing protein	1.24	2.08	3.04	5.87	C2 [<i>Medicago truncatula</i>]	
LesAffx.50259.1.S1_at	AT1G78700	brassinosteroid signalling positive regulator-related	1.13	1.07	1.76	2.76	BRASSINAZOLE-RESISTANT 2 protein, putative [<i>Ricinus communis</i>]	
LesAffx.3081.1.S1_at	AT5G35735	auxin-responsive family protein	1.11	1.12	3.32	5.17	putative membrane protein [<i>Solanum tuberosum</i>]	
Les.3574.1.S1_at	AT4G11140	CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA binding / transcription factor	1.12	1.80	3.89	5.94	RecName: Full=Pathogenesis-related genes transcriptional activator PTI6; AltName: Full=PTO-interacting protein 6	Ethylene-triggered signaling
Les.3575.1.S1_at	AT3G23240	ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	3.52	2.79	13.32	30.70	RecName: Full=Pathogenesis-related genes transcriptional activator PTI5; AltName: Full=PTO-interacting protein 5	
Les.4102.1.S1_at	AT3G16770	ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding/ transcription activator/ transcription factor	-1.12	1.42	1.80	4.43	ethylene-binding protein [<i>Lycopersicon esculentum</i>]	
LesAffx.37916.1.S1_at	AT1G09155	AtPP2-B15 (Phloem protein 2-B15); carbohydrate binding	1.12	3.31	12.73	37.69	phloem-specific lectin PP2-like protein [<i>Arabidopsis thaliana</i>]	
Les.3486.1.S1_at	AT5G59790	unknown protein	1.85	1.69	6.11	11.67	auxin-regulated protein [<i>Lycopersicon esculentum</i>]	
LesAffx.344.3.S1_at	AT3G54040	photoassimilate-responsive protein-related	1.61	1.33	5.79	9.21	NtEIG-E80 [<i>Nicotiana tabacum</i>]	

Les.3735.1.S1_at	AT2G29490	ATGSTU1 (GLUTATHIONE S-TRANSFERASE TAU 1); glutathione transferase	2.50	2.77	3.27	5.65	putative glutathione S-transferase T4 [Lycopersicon esculentum]	
LesAffx.22100.1.S1_at	AT5G45710	RHA1 (ROOT HANDEDNESS 1); DNA binding / transcription factor	1.57	2.38	53.20	47.75	Heat shock factor protein, putative [Ricinus communis]	
LesAffx.2889.4.S1_at	AT4G39390	NST-K1 (NUCLEOTIDE SUGAR TRANSPORTER-KT 1); nucleotide-sugar transmembrane transporter	-1.12	1.31	1.77	3.17	NST-K1 (NUCLEOTIDE SUGAR TRANSPORTER-KT 1); nucleotide-sugar transmembrane transporter [Arabidopsis thaliana]	
LesAffx.67017.1.S1_at	AT5G25220	KNAT3 (KNOTTED1-LIKE HOMEobox GENE 3); transcription activator/ transcription factor	6.40	5.62	12.66	31.43	RecName: Full=Homeobox protein knotted-1-like LET12	
Les.5530.1.S1_at	AT5G60800	heavy-metal-associated domain-containing protein	-1.25	2.09	17.22	43.78	metal ion binding protein, putative [Ricinus communis]	
Les.5755.1.S1_at	AT5G61210	SNAP33 (SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	1.00	1.62	2.50	5.08	synaptosomal associated protein, putative [Ricinus communis]	
Les.5090.1.S1_at	AT3G60450	INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078), PRIB5 (InterPro:IPR012398); B	1.39	1.71	2.76	4.83	pRIB5 protein [Arabidopsis thaliana]	
LesAffx.68459.2.S1_at	AT3G28630	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf whorl, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen	1.16	1.30	16.69	40.95	unknown [Populus trichocarpa]	Unknown

		stage, 4 anthe						
Les.5131.1.S1_at	AT5G42050	FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thali	-1.04	1.37	3.65	6.04	n-rich protein, putative [Ricinus communis]	
LesAффx.2934.1.S1_at	AT5G61630	unknown protein	1.09	1.44	3.19	6.63	PREDICTED: hypothetical protein [Vitis vinifera]	
LesAффx.64990.1.S1_at	AT3G56180	unknown protein	1.36	2.13	3.59	5.36	conserved hypothetical protein [Ricinus communis]	
LesAффx.56634.1.S1_at	AT1G76600	unknown protein	1.39	1.77	5.68	17.88	unnamed protein product [Nicotiana tabacum]	
LesAффx.71544.1.S1_at	AT5G11000	unknown protein	1.77	1.77	55.95	58.61	unnamed protein product [Vitis vinifera]	
Les.113.1.S1_at	no hit found	no hit found	1.71	4.33	26.08	106.79	no hits found	
Les.3262.1.A1_at	no hit found	no hit found	-1.02	1.09	1.60	2.22	no hits found	
Les.1806.2.A1_at	no hit found	no hit found	1.18	1.38	2.14	2.84	no hits found	
Les.3334.1.S1_at	no hit found	no hit found	1.01	1.25	1.94	2.67	no hits found	
Les.4429.2.A1_at	no hit found	no hit found	1.30	2.24	3.17	8.38	no hits found	
Les.1826.1.A1_at	no hit found	no hit found	-1.23	2.16	12.42	33.00	no hits found	
Les.1296.1.A1_at	no hit found	no hit found	1.64	2.60	7.42	10.11	no hits found	

Cluster 1 GO:

Tomato Functional Genomics Database (http://ted.bti.cornell.edu/cgi-bin/TFGD/array/GO_analysis.cgi)

Gene Ontology term	Cluster frequency	Genome frequency of use	Raw P-value	Corrected P-value
protein amino acid phosphorylation	13 out of 90 genes, 14.4%	282 out of 10209 genes, 2.8%	0.00000101	0
hormone-mediated signaling	12 out of 90 genes, 13.3%	238 out of 10209 genes, 2.3%	0.00000107	0
detection of hormone stimulus	4 out of 90 genes, 4.4%	12 out of 10209 genes, 0.1%	0.00000264	0
detection of endogenous stimulus	4 out of 90 genes, 4.4%	12 out of 10209 genes, 0.1%	0.00000264	0
detection of chemical stimulus	4 out of 90 genes, 4.4%	15 out of 10209 genes, 0.1%	0.00000715	0
response to bacterium	9 out of 90 genes, 10.0%	156 out of 10209 genes, 1.5%	0.00000885	0
aromatic amino acid family biosynthetic process, prephenate pathway	4 out of 90 genes, 4.4%	17 out of 10209 genes, 0.2%	0.0000123	0
response to other organism	11 out of 90 genes, 12.2%	270 out of 10209 genes, 2.6%	0.0000235	0
phosphorylation	13 out of 90 genes, 14.4%	382 out of 10209 genes, 3.7%	0.0000276	0
regulation of cellular process	25 out of 90 genes, 27.8%	1216 out of 10209 genes, 11.9%	0.0000328	0
detection of brassinosteroid stimulus	3 out of 90 genes, 3.3%	8 out of 10209 genes, 0.1%	0.0000359	0
defense response	12 out of 90 genes, 13.3%	342 out of 10209 genes, 3.3%	0.0000429	0
signal transduction	15 out of 90 genes, 16.7%	523 out of 10209 genes, 5.1%	0.0000466	0
positive regulation of kinase activity	3 out of 90 genes, 3.3%	9 out of 10209 genes, 0.1%	0.0000535	0
positive regulation of protein kinase activity	3 out of 90 genes, 3.3%	9 out of 10209 genes, 0.1%	0.0000535	0
brassinosteroid mediated signaling	4 out of 90 genes, 4.4%	26 out of 10209 genes, 0.3%	0.0000727	0
steroid hormone mediated signaling	4 out of 90 genes, 4.4%	26 out of 10209 genes, 0.3%	0.0000727	0
positive regulation of transferase activity	3 out of 90 genes, 3.3%	10 out of 10209 genes, 0.1%	0.000076	0.00444
response to hormone stimulus	13 out of 90 genes, 14.4%	425 out of 10209 genes, 4.2%	0.0000829	0.00526
regulation of biological process	25 out of 90 genes, 27.8%	1288 out of 10209 genes, 12.6%	0.0000859	0.005
response to biotic stimulus	11 out of 90 genes, 12.2%	312 out of 10209 genes, 3.1%	0.000088	0.00476

phosphate metabolic process	13 out of 90 genes, 14.4%	434 out of 10209 genes, 4.3%	0.0001	0.00455
intracellular signaling cascade	13 out of 90 genes, 14.4%	434 out of 10209 genes, 4.3%	0.0001	0.00435
phosphorus metabolic process	13 out of 90 genes, 14.4%	435 out of 10209 genes, 4.3%	0.0001	0.00417
cell communication	15 out of 90 genes, 16.7%	562 out of 10209 genes, 5.5%	0.0001	0.004
post-translational protein modification	13 out of 90 genes, 14.4%	439 out of 10209 genes, 4.3%	0.00011	0.00385
detection of stimulus	5 out of 90 genes, 5.6%	56 out of 10209 genes, 0.5%	0.00012	0.0037
defense response to bacterium	7 out of 90 genes, 7.8%	128 out of 10209 genes, 1.3%	0.00013	0.00357
camalexin biosynthetic process	3 out of 90 genes, 3.3%	12 out of 10209 genes, 0.1%	0.00013	0.00345
camalexin metabolic process	3 out of 90 genes, 3.3%	12 out of 10209 genes, 0.1%	0.00013	0.00333
multi-organism process	11 out of 90 genes, 12.2%	333 out of 10209 genes, 3.3%	0.00015	0.00387
response to steroid hormone stimulus	4 out of 90 genes, 4.4%	32 out of 10209 genes, 0.3%	0.00016	0.00375
indole phytoalexin biosynthetic process	3 out of 90 genes, 3.3%	13 out of 10209 genes, 0.1%	0.00017	0.00364
indole metabolic process	3 out of 90 genes, 3.3%	13 out of 10209 genes, 0.1%	0.00017	0.00353
indole phytoalexin metabolic process	3 out of 90 genes, 3.3%	13 out of 10209 genes, 0.1%	0.00017	0.00343
phytoalexin metabolic process	3 out of 90 genes, 3.3%	13 out of 10209 genes, 0.1%	0.00017	0.00333
phytoalexin biosynthetic process	3 out of 90 genes, 3.3%	13 out of 10209 genes, 0.1%	0.00017	0.00324
biological regulation	26 out of 90 genes, 28.9%	1445 out of 10209 genes, 14.2%	0.0002	0.00316
response to endogenous stimulus	13 out of 90 genes, 14.4%	468 out of 10209 genes, 4.6%	0.00021	0.00308
L-phenylalanine biosynthetic process	3 out of 90 genes, 3.3%	14 out of 10209 genes, 0.1%	0.00022	0.003
brassinosteroid homeostasis	3 out of 90 genes, 3.3%	14 out of 10209 genes, 0.1%	0.00022	0.00293
MAPKKK cascade during osmolarity sensing	2 out of 90 genes, 2.2%	3 out of 10209 genes, 0.0%	0.00022	0.00286
activation of MAPK activity during osmolarity sensing	2 out of 90 genes, 2.2%	3 out of 10209 genes, 0.0%	0.00022	0.00279
osmosensory signaling pathway	2 out of 90 genes, 2.2%	3 out of 10209 genes, 0.0%	0.00022	0.00273
response to chitin	5 out of 90 genes, 5.6%	66 out of 10209 genes, 0.6%	0.00027	0.00267
regulation of kinase activity	3 out of 90 genes, 3.3%	15 out of 10209 genes, 0.1%	0.00027	0.00261
regulation of protein kinase activity	3 out of 90 genes, 3.3%	15 out of 10209 genes, 0.1%	0.00027	0.00255
response to brassinosteroid stimulus	4 out of 90 genes, 4.4%	37 out of 10209 genes, 0.4%	0.00029	0.0025
regulation of transferase activity	3 out of 90 genes, 3.3%	16 out of 10209 genes, 0.2%	0.00034	0.00245

response to chemical stimulus	18 out of 90 genes, 20.0%	849 out of 10209 genes, 8.3%	0.00037	0.0024
response to stimulus	27 out of 90 genes, 30.0%	1592 out of 10209 genes, 15.6%	0.0004	0.00275
protein modification process	13 out of 90 genes, 14.4%	499 out of 10209 genes, 4.9%	0.0004	0.00269
vascular transport	2 out of 90 genes, 2.2%	4 out of 10209 genes, 0.0%	0.00045	0.00377
phloem transport	2 out of 90 genes, 2.2%	4 out of 10209 genes, 0.0%	0.00045	0.0037
response to abiotic stimulus	15 out of 90 genes, 16.7%	649 out of 10209 genes, 6.4%	0.0005	0.00364
biopolymer modification	13 out of 90 genes, 14.4%	517 out of 10209 genes, 5.1%	0.00056	0.00357
detection of biotic stimulus	3 out of 90 genes, 3.3%	19 out of 10209 genes, 0.2%	0.00057	0.00351
detection of bacterium	3 out of 90 genes, 3.3%	19 out of 10209 genes, 0.2%	0.00057	0.00345
cellular aromatic compound metabolic process	8 out of 90 genes, 8.9%	218 out of 10209 genes, 2.1%	0.00065	0.00339
activation of MAPK activity	2 out of 90 genes, 2.2%	5 out of 10209 genes, 0.0%	0.00075	0.00567
leaf vascular tissue pattern formation	2 out of 90 genes, 2.2%	5 out of 10209 genes, 0.0%	0.00075	0.00557
positive regulation of MAP kinase activity	2 out of 90 genes, 2.2%	5 out of 10209 genes, 0.0%	0.00075	0.00548
L-phenylalanine metabolic process	3 out of 90 genes, 3.3%	21 out of 10209 genes, 0.2%	0.00078	0.00571
positive regulation of catalytic activity	3 out of 90 genes, 3.3%	22 out of 10209 genes, 0.2%	0.0009	0.00656
abscisic acid mediated signaling	4 out of 90 genes, 4.4%	51 out of 10209 genes, 0.5%	0.00102	0.00708
aromatic amino acid family biosynthetic process	4 out of 90 genes, 4.4%	52 out of 10209 genes, 0.5%	0.0011	0.00818
chorismate metabolic process	4 out of 90 genes, 4.4%	52 out of 10209 genes, 0.5%	0.0011	0.00806
indole derivative biosynthetic process	3 out of 90 genes, 3.3%	25 out of 10209 genes, 0.2%	0.00132	0.00882
positive regulation of flower development	3 out of 90 genes, 3.3%	26 out of 10209 genes, 0.3%	0.00148	0.00957
positive regulation of post-embryonic development	3 out of 90 genes, 3.3%	26 out of 10209 genes, 0.3%	0.00148	0.00943
positive regulation of developmental process	4 out of 90 genes, 4.4%	57 out of 10209 genes, 0.6%	0.00156	0.0107
jasmonic acid and ethylene-dependent systemic resistance, jasmonic acid mediated signaling pathway	2 out of 90 genes, 2.2%	7 out of 10209 genes, 0.1%	0.00156	0.01278
regulation of MAP kinase activity	2 out of 90 genes, 2.2%	7 out of 10209 genes, 0.1%	0.00156	0.0126
MAPKKK cascade	2 out of 90 genes, 2.2%	8 out of 10209 genes, 0.1%	0.00207	0.01595
aromatic amino acid family metabolic process	4 out of 90 genes, 4.4%	62 out of 10209 genes, 0.6%	0.00213	0.016
response to stress	19 out of 90 genes, 21.1%	1077 out of 10209 genes, 10.5%	0.00231	0.01658
indole and derivative metabolic process	3 out of 90 genes, 3.3%	31 out of 10209 genes, 0.3%	0.00249	0.0174

indole derivative metabolic process	3 out of 90 genes, 3.3%	31 out of 10209 genes, 0.3%	0.00249	0.01718
response to fungus	4 out of 90 genes, 4.4%	71 out of 10209 genes, 0.7%	0.00349	0.02759
response to UV	4 out of 90 genes, 4.4%	73 out of 10209 genes, 0.7%	0.00386	0.02875
regulation of transcription, DNA-dependent	11 out of 90 genes, 12.2%	504 out of 10209 genes, 4.9%	0.00462	0.03358
jasmonic acid mediated signaling pathway	3 out of 90 genes, 3.3%	39 out of 10209 genes, 0.4%	0.00481	0.0361
innate immune response	5 out of 90 genes, 5.6%	126 out of 10209 genes, 1.2%	0.00503	0.03614
response to external stimulus	7 out of 90 genes, 7.8%	240 out of 10209 genes, 2.4%	0.00518	0.03762
response to carbohydrate stimulus	5 out of 90 genes, 5.6%	127 out of 10209 genes, 1.2%	0.0052	0.03718
regulation of RNA metabolic process	11 out of 90 genes, 12.2%	514 out of 10209 genes, 5.0%	0.00535	0.03674
defense response, incompatible interaction	4 out of 90 genes, 4.4%	80 out of 10209 genes, 0.8%	0.00536	0.03655
developmental process	14 out of 90 genes, 15.6%	752 out of 10209 genes, 7.4%	0.00585	0.04295
response to osmotic stress	7 out of 90 genes, 7.8%	246 out of 10209 genes, 2.4%	0.00592	0.04247
cell surface receptor linked signal transduction	3 out of 90 genes, 3.3%	43 out of 10209 genes, 0.4%	0.00633	0.044
auxin mediated signaling pathway	4 out of 90 genes, 4.4%	85 out of 10209 genes, 0.8%	0.00664	0.04659
plant-type hypersensitive response	3 out of 90 genes, 3.3%	44 out of 10209 genes, 0.4%	0.00675	0.04674
host programmed cell death induced by symbiont	3 out of 90 genes, 3.3%	44 out of 10209 genes, 0.4%	0.00675	0.04624
regulation of catalytic activity	4 out of 90 genes, 4.4%	86 out of 10209 genes, 0.8%	0.00692	0.04638
immune response	5 out of 90 genes, 5.6%	136 out of 10209 genes, 1.3%	0.00693	0.04589
detection of external stimulus	3 out of 90 genes, 3.3%	45 out of 10209 genes, 0.4%	0.00719	0.04583
programmed cell death	4 out of 90 genes, 4.4%	87 out of 10209 genes, 0.9%	0.0072	0.04557
aromatic compound biosynthetic process	5 out of 90 genes, 5.6%	138 out of 10209 genes, 1.4%	0.00736	0.0451

Cluster 2 genes.

Probe set ID	ATH best hit	Bet hit description	FC 0hr	FC 1 hr	FC 3 hr	FC 5 hr	Gene bank best hit description
Les.5267.1.S1_at	AT5G18480	PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	1.16	1.31	1.59	3.50	glycogenin, putative [Ricinus communis]
Les.4482.1.S1_at	AT4G13010	oxidoreductase, zinc-binding dehydrogenase family protein	1.40	1.66	2.56	5.97	ripening regulated protein-like [Solanum tuberosum]
Les.3712.1.S1_at	AT2G43120	pirin, putative	2.55	1.20	8.76	141.04	RecName: Full=Pirin-like protein
LesAffx.64831.1.S1_at	AT3G26020	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	1.41	1.35	1.92	3.80	protein phosphatase 2A regulatory subunit B' [Zea mays]
Les.176.1.S1_at	AT1G02130	ARA-5 (ARABIDOPSIS RAS 5); GTP binding	-1.09	1.27	1.91	3.62	small GTP-binding protein
LesAffx.62138.1.S1_at	AT5G49620	AtMYB78 (myb domain protein 78); DNA binding / transcription factor	1.12	1.15	2.66	18.23	Cpm5 [Craterostigma plantagineum]
LesAffx.64689.1.S1_at	AT3G59660	C2 domain-containing protein / GRAM domain-containing protein	1.42	1.72	2.35	10.91	PREDICTED: similar to C2 domain-containing protein / GRAM domain-containing protein [Vitis vinifera]
LesAffx.61402.2.S1_at	AT2G19570	CDA1 (CYTIDINE DEAMINASE 1); cytidine deaminase	-1.03	-1.08	2.81	8.71	cytidine deaminase 1, 2, 7, putative [Ricinus communis]
LesAffx.54536.1.S1_at	AT2G29720	CTF2B; monooxygenase/ oxidoreductase	1.46	1.05	2.99	12.05	CTF2B [Arabidopsis thaliana]
LesAffx.38821.1.S1_at	AT4G37310	CYP81H1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygenbinding	1.92	1.48	7.94	32.57	cytochrome P450, putative [Ricinus communis]
LesAffx.23884.1.S1_at	AT2G37820	DC1 domain-containing protein	1.38	1.34	11.20	39.29	DC1 domain-containing protein [Arabidopsis thaliana]

LesAffx.3059.1.S1_at	AT3G23220	DNA binding / transcription factor	-1.04	1.26	17.05	56.27	Ethylene-responsive transcription factor, putative [<i>Ricinus communis</i>]
Les.3818.1.S1_at	AT3G23240	ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/transcription factor	1.08	1.02	3.80	19.91	ethylene responsive element binding protein [<i>Lycopersicon esculentum</i>]
Les.3662.1.S1_at	AT1G01480	ACS2; 1-aminocyclopropane-1-carboxylate synthase	4.65	1.62	25.75	100.57	RecName: Full=1-aminocyclopropane-1-carboxylate synthase 2; Short=ACC synthase 2; AltName: Full=Le-ACS2; Short=ACS-2; AltName: Full=S-adenosyl-L-methionine methylthioadenosine-lyase 2
Les.4623.1.S1_at	AT2G02370	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (In	1.04	1.29	1.64	3.17	PREDICTED: hypothetical protein [<i>Vitis vinifera</i>]
Les.2668.1.S1_at	AT1G59500	GH3.4; indole-3-acetic acid amido synthetase	1.49	-1.00	8.55	10.76	auxin and ethylene responsive GH3-like protein [<i>Capsicum chinense</i>]
Les.966.1.S1_at	AT1G09560	GLP5 (GERMIN-LIKE PROTEIN 5); manganese ion binding / nutrient reservoir	1.25	1.38	2.20	5.51	germin-like protein [<i>Solanum tuberosum</i>]
Les.5092.1.S1_at	AT3G06350	MEE32 (MATERNAL EFFECT EMBRYO ARREST 32); 3-dehydroquinate dehydratase/ NADP or NADPH binding / binding / catalytic/ shikimate 5-dehydrogenase	1.10	-1.19	4.83	15.40	3-dehydroquinate dehydratase / shikimate dehydrogenase isoform 2 [<i>Nicotiana tabacum</i>]
LesAffx.42561.1.S1_at	AT5G15460	MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD)	1.22	1.93	2.48	4.95	MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2) [<i>Arabidopsis thaliana</i>]

		PROTEIN 2)					
LesAffx.12670.1.S1_at	AT2G38060	PHT4;2 (PHOSPHATE TRANSPORTER 4;2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter/ sugar:hydrogen symporter	1.09	1.32	12.30	18.43	Sialin, putative [Ricinus communis]
LesAffx.12670.3.S1_at	AT2G38060	PHT4;2 (PHOSPHATE TRANSPORTER 4;2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter/ sugar:hydrogen symporter	1.06	-1.23	37.48	81.25	Sialin, putative [Ricinus communis]
Les.3493.1.S1_at	AT2G42010	PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D	2.00	2.12	7.28	20.66	phospholipase PLDb1 [Lycopersicon esculentum]
LesAffx.3554.1.A1_at	AT4G37050	PLP4 (PATATIN-LIKE PROTEIN 4); nutrient reservoir	1.24	1.55	4.95	34.60	patatin-like protein 3 [Nicotiana tabacum]
LesAffx.15898.2.S1_at	AT1G05680	UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.16	-1.06	3.09	3.39	UDP-xylose phenolic glycosyltransferase [Solanum lycopersicum]
LesAffx.61149.1.S1_at	AT5G49690	UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.08	1.25	2.52	5.41	UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]
Les.5481.1.S1_at	AT4G14420	lesion inducing protein-related	1.22	1.38	1.34	2.90	ORF; able to induce HR-like lesions [Nicotiana tabacum]
LesAffx.56130.1.S1_at	AT1G25390	protein kinase family protein	2.02	-1.02	6.80	20.48	wall-associated kinase, putative [Ricinus communis]
Les.3418.1.S1_at	AT3G01980	short-chain dehydrogenase/reductase (SDR) family protein	1.21	1.50	2.24	4.89	short-chain alcohol dehydrogenase [Panax ginseng]

Les.4885.1.S1_at	AT2G39980	transferase family protein	2.37	1.02	16.53	148.30	AER [Nicotiana tabacum]
LesAffx.43640.1.S1_at	AT4G18530	unknown protein	1.48	1.11	1.22	4.50	conserved hypothetical protein [Ricinus communis]
LesAffx.15850.1.S1_a_at	AT1G67060	unknown protein	1.31	-1.43	4.21	11.11	unknown protein [Arabidopsis thaliana]
LesAffx.65135.1.S1_at	AT1G28700	unknown protein	1.58	1.59	7.60	47.70	pentatricopeptide repeat-containing protein, putative [Ricinus communis]
Les.3418.2.S1_a_at	no hits found	unknown protein	1.41	1.43	2.52	5.23	no hits found
Les.2746.2.A1_at	no hits found	unknown protein	1.54	2.36	5.59	67.42	no hits found

Cluster 2 GO:

AtCOSCiS (<http://bioinformatics.psb.ugent.be/ATCOECIS/>)

GO enrichment	Enrichment fold	p-value	Description
GO:0009873	34.51 (2)	1.54E-03	Ethylene mediated signaling pathway
GO:0045735	27.30 (2)	2.45E-03	Nutrient reservoir activity
GO:0000160	25.40 (2)	2.82E-03	Two-component signal transduction system (phosphorelay)
GO:0009723	13.85 (2)	9.15E-03	Response to ethylene stimulus
GO:0009755	9.28 (2)	1.96E-02	Hormone-mediated signaling
GO:0042829	8.09 (2)	2.53E-02	Defense response to pathogen
GO:0009814	8.09 (2)	2.53E-02	Defense response to pathogen, incompatible interaction
GO:0042828	8.09 (2)	2.53E-02	Response to pathogen
GO:0016758	7.65 (2)	2.80E-02	Transferase activity, transferring hexosyl groups
GO:0009613	7.09 (2)	3.22E-02	Response to pest, pathogen or parasite
GO:0016757	6.22 (3)	1.21E-02	Transferase activity, transferring glycosyl groups
GO:0009725	5.92 (4)	4.39E-03	Response to hormone stimulus
GO:0009719	4.21 (4)	1.42E-02	Response to endogenous stimulus
GO:0051707	4.01 (2)	8.84E-02	Response to other organism
GO:0007242	3.95 (2)	9.07E-02	Intracellular signaling cascade
GO:0006950	3.44 (4)	2.75E-02	Response to stress
GO:0042221	3.27 (4)	3.26E-02	Response to chemical stimulus
GO:0007165	3.25 (3)	6.35E-02	Signal transduction
GO:0007154	2.99 (3)	7.77E-02	Cell communication
GO:0006118	2.97 (2)	1.45E-01	Electron transport
GO:0006355	2.95 (3)	8.03E-02	Regulation of transcription, DNA-dependent

Cluster 3 genes.

Probe set ID	ATH best hit	Bet hit description	FC 0hr	FC 1hr	FC 3hr	FC 5 hr	Gene bank best hit description
Les.3039.1.S1_at	AT1G22410	2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative	1.38	1.46	2.09	3.70	RecName: Full=Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic; AltName: Full=Phospho-2-keto-3-deoxyheptonate aldolase 2; AltName: Full=3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2; AltName: Full=DAHP synthetase 2; Flags: Precursor
LesAffx.62420.1.S1_at	AT2G15480	UGT73B5 (UDP-glucosyl transferase 73B5); UDP-glucosyltransferase/ UDP-glucosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	4.32	1.84	6.96	16.48	UDP-glucose:glucosyltransferase [Lycium barbarum]
LesAffx.11941.1.S1_at	AT3G49340	cysteine proteinase, putative	1.66	1.84	1.75	2.34	phytophthora-inhibited protease 1 [Solanum lycopersicum]
Les.3672.1.S1_at	AT2G45300	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate/ EPSP synthase	-1.17	1.29	1.21	2.24	RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Flags: Precursor
Les.2817.1.S1_at	AT1G10670	ACLA-1; ATP citrate synthase	1.32	1.30	1.92	2.87	ATP-citrate synthase, putative [Ricinus communis]
Les.37.1.S1_at	AT3G12500	ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	7.23	5.47	6.60	6.79	RecName: Full=Basic endochitinase
LesAffx.18587.1.S1_at	AT5G16080	AtCXE17 (Arabidopsis thaliana carboxyesterase 17); hydrolase	1.81	1.70	2.52	2.59	hsr203J [Solanum tuberosum]
LesAffx.19956.1.S1_at	AT3G29200	CM1 (CHORISMATE MUTASE 1); L-ascorbate peroxidase/ chorismate mutase	-1.23	1.22	1.34	2.70	putative chorismate mutase 1 [Capsicum annuum]
LesAffx.44563.1.A1_at	AT1G69370	CM3 (chorismate mutase 3); chorismate mutase	-1.14	1.43	1.46	2.72	putative chorismate mutase 1 [Capsicum annuum]

LesAffx.9038.3.S1_at	AT4G37400	CYP81F3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygenbinding	2.07	1.78	2.65	5.08	CYP81B2v2 [Nicotiana tabacum]
Les.209.1.S1_at	AT1G48850	EMB1144 (embryo defective 1144); chorismate synthase	-1.10	1.18	1.18	2.08	RecName: Full=Chorismate synthase 1, chloroplastic; AltName: Full=5-enolpyruylshikimate-3-phosphate phospholyase 1; Flags: Precursor
Les.3774.1.S1_at	AT5G26340	MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	3.66	2.72	2.80	2.89	hexose transporter [Solanum lycopersicum]
LesAffx.62349.1.S1_at	AT3G27890	NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase	2.24	2.16	2.01	3.49	RecName: Full=NAD(P)H:quinone oxidoreductase; Short=NAD(P)H:QR
Les.2747.1.S1_at	AT5G48880	PKT2 (PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 2); acetyl-CoA C-acyltransferase/ catalytic	1.40	1.77	2.65	2.70	PKT2 (PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 2); acetyl-CoA C-acyltransferase/ catalytic [Arabidopsis thaliana]
Les.2747.2.S1_at	AT2G33150	PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase	1.46	1.68	3.04	2.96	3-ketoacyl CoA thiolase 1 [Petunia x hybrida]
Les.3140.3.S1_at	AT2G33150	PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase	1.65	1.68	3.10	2.89	3-ketoacyl CoA thiolase 1 [Petunia x hybrida]
Les.3140.2.S1_at	AT2G33150	PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase	1.42	1.72	3.10	2.80	3-ketoacyl CoA thiolase 1 [Petunia x hybrida]
LesAffx.71598.1.S1_at	AT1G75170	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	1.40	1.88	1.97	2.15	transporter-like protein [Solanum tuberosum]
Les.4880.1.S1_at	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	2.75	2.31	4.03	4.62	elicitor-inducible cytochrome P450 [Nicotiana tabacum]
LesAffx.9043.1.S1_at	AT2G47650	UXS4 (UDP-XYLOSE SYNTHASE 4); UDP-	1.28	1.11	1.87	2.52	putative UDP-glucuronate decarboxylase 3 [Nicotiana

		glucuronate decarboxylase/ catalytic					tabacum]
LesAffx.10235.1.S1_at	AT1G66120	acyl-activating enzyme 11 (AAE11)	1.42	3.70	3.91	3.12	acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]
LesAffx.16769.1.S1_at	AT1G65870	disease resistance-responsive family protein	4.75	2.79	3.21	3.27	dirigent-like protein pDIR10 [Picea glauca]
LesAffx.51292.1.S1_at	AT5G35200	epsin N-terminal homology (ENTH) domain-containing protein	-1.10	1.25	1.53	2.55	ANTH [Medicago truncatula]
LesAffx.6163.2.S1_at	AT5G52810	ornithine cyclodeaminase/mu- crystallin family protein	1.25	1.52	2.12	2.31	ornithine cyclodeaminase, putative [Ricinus communis]
Les.3635.1.S1_at	AT2G05920	subtilase family protein	1.81	1.95	2.04	2.22	subtilisin-like protease [Solanum lycopersicum]
Les.2529.2.S1_at	AT5G17540	transferase family protein	1.47	1.52	3.09	3.31	benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Petunia x hybrida]
LesAffx.60643.2.S1_at	AT1G67850	unknown protein	1.65	1.47	1.27	2.51	putative lysine ketoglutarate reductase trans-splicing related 1 [Oryza sativa Japonica Group]
LesAffx.60643.1.S1_at	AT1G08040	unknown protein	1.37	1.44	1.30	2.35	lysine ketoglutarate reductase trans-splicing related 1 [Zea mays]
Les.2587.1.A1_at			1.34	2.22	1.88	3.73	no hits found
Les.1590.1.A1_at			1.13	1.33	1.50	2.07	no hits found
Les.2529.1.A1_at			1.41	1.65	2.51	2.58	HRS201-like protein [Solanum melongena]

Cluster 3 GO:

Tomato Functional Genomics Database (http://ted.bti.cornell.edu/cgi-bin/TFGD/array/GO_analysis.cgi)

Gene Ontology term	Cluster frequency	Genome frequency of use	Raw P-value	Corrected P-value
glyoxysome organization	4 out of 31 genes, 12.9%	6 out of 10209 genes, 0.1%	1.03E-09	0
jasmonic acid biosynthetic process	4 out of 31 genes, 12.9%	17 out of 10209 genes, 0.2%	1.61E-07	0
aromatic amino acid family biosynthetic process	5 out of 31 genes, 16.1%	52 out of 10209 genes, 0.5%	4.32E-07	0
chorismate metabolic process	5 out of 31 genes, 16.1%	52 out of 10209 genes, 0.5%	4.32E-07	0
jasmonic acid metabolic process	4 out of 31 genes, 12.9%	22 out of 10209 genes, 0.2%	4.89E-07	0
fatty acid beta-oxidation	4 out of 31 genes, 12.9%	23 out of 10209 genes, 0.2%	5.91E-07	0
oxylipin biosynthetic process	4 out of 31 genes, 12.9%	23 out of 10209 genes, 0.2%	5.91E-07	0
fatty acid oxidation	4 out of 31 genes, 12.9%	26 out of 10209 genes, 0.3%	9.92E-07	0
lipid oxidation	4 out of 31 genes, 12.9%	26 out of 10209 genes, 0.3%	9.92E-07	0
aromatic amino acid family metabolic process	5 out of 31 genes, 16.1%	62 out of 10209 genes, 0.6%	1.05E-06	0
fatty acid catabolic process	4 out of 31 genes, 12.9%	27 out of 10209 genes, 0.3%	1.16E-06	0
oxylipin metabolic process	4 out of 31 genes, 12.9%	28 out of 10209 genes, 0.3%	1.35E-06	0
jasmonic acid and ethylene-dependent systemic resistance	4 out of 31 genes, 12.9%	30 out of 10209 genes, 0.3%	1.80E-06	0
organic acid catabolic process	4 out of 31 genes, 12.9%	30 out of 10209 genes, 0.3%	1.80E-06	0
carboxylic acid catabolic process	4 out of 31 genes, 12.9%	30 out of 10209 genes, 0.3%	1.80E-06	0
cellular lipid catabolic process	4 out of 31 genes, 12.9%	32 out of 10209 genes, 0.3%	2.35E-06	0
lipid modification	4 out of 31 genes, 12.9%	34 out of 10209 genes, 0.3%	3.02E-06	0
aromatic compound biosynthetic process	6 out of 31 genes, 19.4%	138 out of 10209 genes, 1.4%	3.05E-06	0
plastid organization	4 out of 31 genes, 12.9%	42 out of 10209 genes, 0.4%	7.18E-06	0
dicarboxylic acid metabolic process	5 out of 31 genes, 16.1%	98 out of 10209 genes, 1.0%	1.02E-05	0
carboxylic acid metabolic process	9 out of 31 genes, 29.0%	548 out of 10209 genes, 5.4%	2.41E-05	0
organic acid metabolic process	9 out of 31 genes, 29.0%	550 out of 10209 genes, 5.4%	2.48E-05	0
cellular aromatic compound metabolic process	6 out of 31 genes, 19.4%	218 out of 10209 genes, 2.1%	4.16E-05	0
organic acid biosynthetic process	5 out of 31 genes, 16.1%	144 out of 10209 genes, 1.4%	6.58E-05	0.00083

carboxylic acid biosynthetic process	5 out of 31 genes, 16.1%	144 out of 10209 genes, 1.4%	6.58E-05	0.0008
lipid catabolic process	4 out of 31 genes, 12.9%	78 out of 10209 genes, 0.8%	8.48E-05	0.00077
defense response, incompatible interaction	4 out of 31 genes, 12.9%	80 out of 10209 genes, 0.8%	9.36E-05	0.00074
amino acid biosynthetic process	5 out of 31 genes, 16.1%	159 out of 10209 genes, 1.6%	0.0001	0.00071
fatty acid biosynthetic process	4 out of 31 genes, 12.9%	98 out of 10209 genes, 1.0%	0.0002	0.00138
amine biosynthetic process	5 out of 31 genes, 16.1%	191 out of 10209 genes, 1.9%	0.00024	0.00133
nitrogen compound biosynthetic process	5 out of 31 genes, 16.1%	197 out of 10209 genes, 1.9%	0.00028	0.00129
defense response	6 out of 31 genes, 19.4%	342 out of 10209 genes, 3.3%	0.00048	0.00313
response to wounding	4 out of 31 genes, 12.9%	126 out of 10209 genes, 1.2%	0.00053	0.00364
innate immune response	4 out of 31 genes, 12.9%	126 out of 10209 genes, 1.2%	0.00053	0.00353
fatty acid metabolic process	4 out of 31 genes, 12.9%	136 out of 10209 genes, 1.3%	0.00071	0.00514
immune response	4 out of 31 genes, 12.9%	136 out of 10209 genes, 1.3%	0.00071	0.005
immune system process	4 out of 31 genes, 12.9%	152 out of 10209 genes, 1.5%	0.00108	0.00649
cellular amino acid and derivative metabolic process	6 out of 31 genes, 19.4%	403 out of 10209 genes, 3.9%	0.00115	0.00632
response to other organism	5 out of 31 genes, 16.1%	270 out of 10209 genes, 2.6%	0.0012	0.00615
organelle organization	5 out of 31 genes, 16.1%	271 out of 10209 genes, 2.7%	0.00122	0.006
amino acid metabolic process	5 out of 31 genes, 16.1%	279 out of 10209 genes, 2.7%	0.00139	0.00585
response to biotic stimulus	5 out of 31 genes, 16.1%	312 out of 10209 genes, 3.1%	0.00228	0.01048
cellular amine metabolic process	5 out of 31 genes, 16.1%	320 out of 10209 genes, 3.1%	0.00254	0.01023
cellular nitrogen compound metabolic process	5 out of 31 genes, 16.1%	329 out of 10209 genes, 3.2%	0.00287	0.01136
multi-organism process	5 out of 31 genes, 16.1%	333 out of 10209 genes, 3.3%	0.00302	0.01156
nitrogen compound metabolic process	5 out of 31 genes, 16.1%	359 out of 10209 genes, 3.5%	0.00418	0.01783
lipid biosynthetic process	4 out of 31 genes, 12.9%	231 out of 10209 genes, 2.3%	0.00497	0.02085
cellular biosynthetic process	11 out of 31 genes, 35.5%	1599 out of 10209 genes, 15.7%	0.00546	0.02125
response to external stimulus	4 out of 31 genes, 12.9%	240 out of 10209 genes, 2.4%	0.00569	0.02204
monocarboxylic acid metabolic process	4 out of 31 genes, 12.9%	244 out of 10209 genes, 2.4%	0.00603	0.024
metabolic process	19 out of 31 genes, 61.3%	3836 out of 10209 genes, 37.6%	0.0062	0.02471
cellular component organization	6 out of 31 genes, 19.4%	565 out of 10209 genes, 5.5%	0.00629	0.02423
biosynthetic process	11 out of 31 genes, 35.5%	1673 out of 10209 genes, 16.4%	0.00774	0.02868

Cluster 4 genes.

Probe set ID	ATH best hit	Bet hit description	FC 0hr	FC 1hr	FC 3hr	FC 5hr	Gene bank best hit description
Les.1524.1.A1_at			1.04	-1.33	1.80	4.50	no hits found
Les.1297.2.A1_at			1.43	1.11	2.58	4.18	no hits found
Les.4045.1.S1_at			1.29	10.56	2.56	3.74	no hits found
Les.2717.1.S1_at	AT3G48140	senescence-associated protein, putative	1.13	1.64	1.80	3.52	B12D-like protein [Beta vulgaris]
Les.2717.2.A1_at			1.11	1.93	1.68	3.37	no hits found
Les.4566.1.S1_at	AT1G09770	ATCDC5 (ARABIDOPSIS THALIANA CELL DIVISION CYCLE 5); DNA binding / transcription factor	-1.54	-1.43	-1.64	-2.01	CDC5-like protein [Solanum lycopersicum]
Les.2230.1.A1_at			-1.17	1.08	-1.21	-2.01	no hits found
Les.2820.2.S1_at	AT3G29320	glucan phosphorylase, putative	-1.28	-1.39	-1.15	-2.01	RecName: Full=Alpha-1,4 glucan phosphorylase L-1 isozyme, chloroplastic/amloplastic; AltName: Full=Starch phosphorylase L-1; Flags: Precursor
Les.32.1.S1_at	AT4G08920	CRY1 (CRYPTOCHROME 1); ATP binding / blue light photoreceptor/ protein homodimerization/ protein kinase	-1.40	1.10	-1.25	-2.02	cryptochrome 1 [Lycopersicon esculentum]
Les.5307.1.S1_at	AT3G56930	zinc finger (DHHC type) family protein	-1.36	1.09	-1.09	-2.03	zinc finger protein, putative [Ricinus communis]
Les.5108.1.S1_at	AT4G22140	DNA binding / protein binding / zinc ion binding	-1.27	1.49	-1.33	-2.03	phd finger transcription factor, putative [Ricinus communis]
LesAffx.35132.1.S1_at	AT1G54500	rubredoxin family protein	-1.21	1.07	-1.10	-2.05	putative rubredoxin [Musa acuminata]
LesAffx.68801.1.S1_at	AT5G52580	RAB GTPase activator	-1.31	-2.02	-1.32	-2.06	RAB GTPase activator [Arabidopsis thaliana]
LesAffx.55680.1.S1_at	AT5G64380	fructose-1,6-bisphosphatase family protein	-1.14	-1.14	-1.04	-2.07	fructose-1,6-bisphosphatase, putative [Ricinus communis]
Les.1598.1.S1_at	AT3G58800	unknown protein	-1.27	1.56	-1.25	-2.09	unnamed protein product [Vitis vinifera]
Les.2327.1.A1_at			-1.16	1.01	-1.01	-2.10	no hits found
Les.2991.2.S1_at			-1.13	-1.51	-1.31	-2.10	no hits found
Les.4834.1.S1_at	AT1G43710	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding	1.02	1.22	-1.06	-2.11	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]
Les.181.1.A1_at			-1.15	1.26	-1.12	-2.12	no hits found
LesAffx.31317.11.S1_at	AT1G64940	CYP89A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen-	-1.41	-1.08	-1.22	-2.15	cytochrome P450 [Capsicum annuum]

		binding					
LesAffx.65412.1.S1_at	AT4G04770	ATABC1 (ATP BINDING CASSETTE PROTEIN 1); ATPase, coupled to transmembrane movement of substances / protein binding / transporter	-1.23	-1.06	-1.16	-2.15	non-intrinsic ABC protein [<i>Nicotiana benthamiana</i>]
LesAffx.36895.1.S1_at	AT3G10970	haloacid dehalogenase-like hydrolase family protein	-1.20	1.12	-1.08	-2.16	haloacid dehalogenase-like hydrolase family protein [<i>Arabidopsis thaliana</i>]
LesAffx.71493.2.S1_at	AT5G07370	IPK2a (INOSITOL POLYPHOSPHATE KINASE 2 ALPHA); inositol or phosphatidylinositol kinase/ inositol trisphosphate 6-kinase	-1.40	1.02	-1.22	-2.17	inositol polyphosphate multikinase [<i>Solanum tuberosum</i>]
Les.2824.1.S1_at	AT3G51840	ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase	-1.25	1.34	-1.29	-2.18	acyl-CoA dehydrogenase, putative [<i>Ricinus communis</i>]
Les.3293.3.S1_at	AT3G48870	HSP93-III; ATP binding / ATPase/ DNA binding / nuclease/ nucleoside-triphosphatase/ nucleotide binding / protein binding	-1.10	-2.02	-1.29	-2.18	RecName: Full=ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B, chloroplastic; Flags: Precursor
Les.5696.1.S1_at	AT1G29700	unknown protein	-1.27	1.11	-1.20	-2.19	Zn-dependent hydrolases of the beta-lactamase fold [<i>Brachypodium sylvaticum</i>]
LesAffx.64239.1.S1_at	AT1G75460	ATP-dependent protease La (LON) domain-containing protein	-1.13	1.27	-1.31	-2.20	ATP-dependent peptidase, putative [<i>Ricinus communis</i>]
LesAffx.33443.1.S1_at	AT1G56180	unknown protein	-1.35	1.40	-1.22	-2.20	PREDICTED: hypothetical protein [<i>Vitis vinifera</i>]
LesAffx.16672.1.S1_at	AT3G63010	GID1B (GA INSENSITIVE DWARF1B); hydrolase	-1.12	1.18	-1.24	-2.21	GID1-5 [<i>Gossypium hirsutum</i>]
Les.4258.3.S1_at	AT5G64940	ATATH13; transporter	-1.28	-1.30	-1.27	-2.22	ATATH13; transporter [<i>Arabidopsis thaliana</i>]
Les.2875.3.S1_at	AT4G38160	pde191 (pigment defective 191)	-1.02	-1.39	-1.23	-2.23	pde191 (pigment defective 191) [<i>Arabidopsis thaliana</i>]
LesAffx.25786.1.S1_at	AT1G54520	unknown protein	-1.44	-1.05	-1.22	-2.26	hypothetical protein [<i>Vitis vinifera</i>]
LesAffx.61588.1.S1_at	AT3G12560	TRFL9 (TRF-LIKE 9); DNA bending/ DNA binding / telomeric DNA binding	-1.28	1.21	-1.29	-2.29	telomere binding protein [<i>Solanum lycopersicum</i>]
Les.4794.1.S1_at	AT1G76990	ACR3; amino acid binding	-1.38	1.02	-1.22	-2.30	amino acid binding protein, putative [<i>Ricinus communis</i>]
LesAffx.65563.1.S1_at	AT5G63490	CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein	-1.54	-1.27	-1.21	-2.32	CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein [<i>Arabidopsis thaliana</i>]
Les.112.1.S1_at	AT5G67030	ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase	-1.47	-1.04	-1.12	-2.33	RecName: Full=Zeaxanthin epoxidase, chloroplastic; Flags: Precursor
Les.3322.3.S1_at	AT5G13630	GUN5 (GENOMES UNCOUPLED 5); magnesium chelatase	-1.35	-1.04	-1.34	-2.35	magnesium chelatase [<i>Capsicum annuum</i>]

LesAffx.1583.1.S1_at	AT3G25805	unknown protein	-1.34	1.13	-1.28	-2.37	hypothetical protein [Vitis vinifera]
LesAffx.39331.1.S1_at	AT4G38160	pde191 (pigment defective 191)	-1.25	1.09	-1.12	-2.37	pde191 (pigment defective 191) [Arabidopsis thaliana]
Les.3488.1.S1_at	AT4G08920	CRY1 (CRYPTOCHROME 1); ATP binding / blue light photoreceptor/ protein homodimerization/ protein kinase	-1.52	1.21	-1.29	-2.37	cryptochrome 1b [Lycopersicon esculentum]
Les.2115.2.S1_at			-1.12	1.52	-1.11	-2.37	no hits found
LesAffx.65209.1.S1_at	AT1G68070	zinc finger (C3HC4-type RING finger) family protein	-1.29	-1.22	-1.02	-2.37	putative RING zinc finger protein [Arabidopsis thaliana]
Les.3522.1.S1_at	AT5G20280	ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase,transferring glycosyl groups	-1.33	-1.03	-1.45	-2.43	sucrose phosphate synthase [Lycopersicon esculentum]
LesAffx.67008.1.S1_at	AT4G20350	unknown protein	-1.13	1.22	-1.20	-2.43	unnamed protein product [Vitis vinifera]
LesAffx.20922.1.S1_at	AT1G68080	iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	-1.45	1.84	-1.19	-2.45	iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana]
Les.4760.1.S1_at	AT2G39950	unknown protein	-1.21	1.09	-1.45	-2.45	unnamed protein product [Vitis vinifera]
Les.5758.1.S1_at	AT5G44250	unknown protein	-1.10	1.07	-1.36	-2.45	PREDICTED: hypothetical protein [Vitis vinifera]
Les.5200.1.S1_at	AT5G11580	UVB-resistance protein-related / regulator of chromosome condensation (RCC1) family protein	-1.20	-1.02	-1.23	-2.46	Protein pim1, putative [Ricinus communis]
Les.3500.1.S1_at	AT1G66340	ETR1 (ETHYLENE RESPONSE 1); ethylene binding / protein histidine kinase/two-component response regulator	-1.13	1.01	-1.13	-2.48	RecName: Full=Ethylene receptor 2; Short=LeETR2
Les.4753.1.S1_at	AT3G50210	2-oxoacid-dependent oxidase, putative	-1.15	-1.03	-1.15	-2.48	putative flavonol synthase-like protein [Euphorbia esula]
Les.631.3.S1_at	AT3G30390	amino acid transporter family protein	-1.44	-1.14	-1.11	-2.49	amino acid transporter [Populus trichocarpa]
Les.2620.3.S1_at	AT1G15740	leucine-rich repeat family protein	-1.03	1.05	-1.07	-2.50	F-box-containing protein 1 [Malus x domestica]
Les.2115.2.S1_a_at			-1.11	1.49	-1.15	-2.50	no hits found
Les.1401.3.S1_at	AT5G18670	BMY3; beta-amylase/ catalytic/ cation binding	-1.10	-1.24	-1.48	-2.52	1,4-alpha-glucan-maltohydrolase [Solanum lycopersicum]
LesAffx.68173.1.S1_at	AT1G04970	lipid-binding serum glycoprotein family protein	-1.28	-1.77	-1.08	-2.54	Lipopolsaccharide-binding protein precursor, putative [Ricinus communis]
Les.1401.2.S1_at	AT5G18670	BMY3; beta-amylase/ catalytic/ cation binding	-1.29	-1.18	-1.47	-2.54	1,4-alpha-glucan-maltohydrolase [Solanum lycopersicum]

Les.1493.1.S1_at	AT5G22300	NIT4 (NITRILASE 4); 3-cyanoalanine hydratase/ cyanoalanine nitrilase/ indole-3-acetonitrile nitrilase/ nitrilase/ nitrile hydratase	-1.54	-1.02	-1.48	-2.57	RecName: Full=Bifunctional nitrilase/nitrile hydratase NIT4B; Short=TNIT4B; AltName: Full=Nitrolase 4B; AltName: Full=Cyanoalanine nitrilase B
LesAffx.67395.1.S1_at	AT5G27320	GID1C (GA INSENSITIVE DWARF1C); hydrolase	-1.04	-1.06	-1.16	-2.58	Gibberellin receptor GID1, putative [Ricinus communis]
Les.2123.2.S1_at	AT3G26100	regulator of chromosome condensation (RCC1) family protein	-1.28	-1.20	-1.07	-2.60	RCC1 and BTB domain-containing protein, putative [Ricinus communis]
Les.1464.1.S1_at	AT5G23050	AAE17 (ACYL-ACTIVATING ENZYME 17); catalytic/ ligase	-1.25	1.03	-1.54	-2.61	acetyl-CoA synthetase, putative [Ricinus communis]
Les.4334.1.A1_at			-1.20	1.67	1.11	-2.61	no hits found
LesAffx.58430.1.S1_at	AT1G22100	ATP binding / inositol pentakisphosphate 2-kinase	-1.55	-1.03	-1.05	-2.62	inositol pentakisphosphate 2-kinase [Glycine max]
Les.2115.1.S1_at	AT1G15340	MBD10; DNA binding / methyl-CpG binding	-1.16	1.49	-1.24	-2.65	MBD10; DNA binding / methyl-CpG binding [Arabidopsis thaliana]
Les.5068.1.S1_at	AT5G23230	NIC2 (NICOTINAMIDASE 2); catalytic/ nicotinamidase	-1.49	1.05	-1.18	-2.69	Isochorismatase, putative [Ricinus communis]
Les.4334.2.S1_at	AT1G73040	jacalin lectin family protein	-1.02	1.39	-1.06	-2.72	jacalin-domain protein [Plantago major]
Les.5354.1.S1_at	AT4G34020	DJ-1 family protein	-1.40	1.15	-1.15	-2.76	DJ-1 family protein [Arabidopsis thaliana]
LesAffx.65080.1.A1_at	AT4G32250	protein kinase family protein	-1.39	1.46	-1.10	-2.76	protein kinase, putative [Ricinus communis]
Les.1977.2.S1_at			-1.23	-1.55	-1.55	-2.77	no hits found
LesAffx.61242.1.S1_at	AT4G36980	unknown protein	1.13	-1.73	-1.27	-2.78	Splicing factor, arginine-serine-rich, putative [Ricinus communis]
LesAffx.17339.1.S1_at	AT1G19870	iqd32 (IQ-domain 32); calmodulin binding	-1.37	-1.08	-1.50	-2.80	iqd32 (IQ-domain 32); calmodulin binding [Arabidopsis thaliana]
LesAffx.66486.1.S1_at	AT3G45620	transducin family protein / WD-40 repeat family protein	-1.31	-1.07	-1.14	-2.82	WD domain containing protein, putative [Solanum demissum]
Les.2493.1.A1_at			-2.30	1.74	-1.39	-2.85	no hits found
LesAffx.50639.1.S1_at	AT5G42210	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Major facilitator superfamily MFS-1 (InterPro:IPR011701), Major facilitator superfamily, general substrate trans	-2.13	-1.07	-1.87	-2.86	Hippocampus abundant transcript 1 protein, putative [Ricinus communis]
LesAffx.55283.1.S1_at	AT3G20910	NF-YA9 (NUCLEAR FACTOR Y, SUBUNIT A9); specific transcriptional repressor/ transcription factor	-1.62	1.35	-1.32	-2.89	YA4 [Antirrhinum majus]

Les.1793.1.A1_at			-1.23	1.17	-1.36	-2.94	no hits found
LesAffx.56656.1.S1_at	AT4G22850	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (In	-1.02	-1.57	-1.46	-2.95	predicted protein [Populus trichocarpa]
Les.3481.1.S1_a_at	AT3G15730	PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D	-1.46	1.01	-1.32	-2.99	phospholipase D [Lycopersicon esculentum]
Les.5344.1.S1_at	AT3G26890	unknown protein	-1.27	1.12	-1.32	-3.01	PREDICTED: hypothetical protein [Vitis vinifera]
LesAffx.62465.1.S1_at	AT5G67385	protein binding / signal transducer	-1.54	-1.12	-1.34	-3.01	Root phototropism protein, putative [Ricinus communis]
Les.32.2.S1_a_at	AT4G08920	CRY1 (CRYPTOCHROME 1); ATP binding / blue light photoreceptor/ protein homodimerization/ protein kinase	-1.49	-1.52	-1.45	-3.02	cryptochrome 1 [Lycopersicon esculentum]
Les.5255.1.S1_at	AT1G21680	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole, plant-type cell wall; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40-like Beta	-1.27	-1.13	-1.24	-3.04	tolB protein-related [Arabidopsis thaliana]
LesAffx.71493.1.S1_at	AT5G61760	ATIPK2BETA; inositol or phosphatidylinositol kinase/ inositol triphosphate 6-kinase	-1.44	-1.14	-1.29	-3.04	inositol polyphosphate multikinase [Solanum tuberosum]
LesAffx.44265.1.S1_at	AT4G00560	methionine adenosyltransferase regulatory beta subunit-related	-1.49	-1.04	-1.21	-3.04	dtdp-4-dehydrorhamnose dehydrogenase, putative [Ricinus communis]
Les.5121.1.S1_at	AT3G47430	PEX11B	-1.21	1.32	-1.47	-3.04	peroxisomal biogenesis factor, putative [Ricinus communis]
LesAffx.21904.1.S1_at	AT1G44446	CH1 (CHLORINA 1); chlorophyllide a oxygenase	-1.49	-1.09	-1.37	-3.08	chlorophyll synthase, putative [Ricinus communis]
LesAffx.70505.1.S1_at	AT3G19860	basic helix-loop-helix (bHLH) family protein	-1.08	-1.50	-2.01	-3.10	DNA binding protein, putative [Ricinus communis]
LesAffx.51346.1.S1_at	AT1G54520	unknown protein	-1.80	-1.45	-1.32	-3.11	PREDICTED: hypothetical protein [Vitis vinifera]
Les.2761.1.A1_at			-1.67	1.39	-1.32	-3.11	no hits found
Les.3322.1.S1_at	AT5G13630	GUN5 (GENOMES UNCOUPLED 5); magnesium chelatase	-1.41	-1.49	-1.43	-3.11	Mg protoporphyrin IX chelatase [Nicotiana tabacum]
Les.2298.2.A1_a_at			-1.62	-1.02	-1.33	-3.14	no hits found

LesAffx.69867.3.S1_at	AT3G62110	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	-2.14	-1.13	-1.71	-3.15	polygalacturonase-like protein-like [Solanum tuberosum]
Les.5311.1.S1_at	AT2G46550	unknown protein	-1.44	1.29	-1.36	-3.29	PREDICTED: hypothetical protein [Vitis vinifera]
Les.5010.1.S1_at	AT3G48110	EDD1 (EMBRYO-DEFECTIVE-DEVELOPMENT 1); glycine-tRNA ligase	-1.13	-2.95	-1.58	-3.32	Glycyl-tRNA synthetase 2, chloroplast/mitochondrial precursor, putative [Ricinus communis]
LesAffx.69782.1.S1_at	AT3G19990	unknown protein	-1.50	-1.50	-1.39	-3.36	predicted protein [Populus trichocarpa]
Les.1064.1.S1_at	AT4G02630	protein kinase family protein	-1.19	1.15	-1.27	-3.36	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Les.5360.1.S1_at	AT1G65660	SMP1 (SWELLMAP 1); nucleic acid binding / single-stranded RNA binding	-1.29	1.15	-1.11	-3.38	step II splicing factor slu7, putative [Ricinus communis]
Les.2594.1.S1_at	AT2G31130	unknown protein	-1.57	-1.01	-1.52	-3.58	fiber protein Fb32 [Gossypium barbadense]
Les.2.1.S1_at	AT2G32810	BGAL9 (Beta galactosidase 9); beta-galactosidase/ catalytic/ cation binding / sugar binding	-1.40	1.03	-1.16	-3.61	beta-galactosidase [Lycopersicon esculentum]
LesAffx.52470.1.S1_at	AT3G22970	unknown protein	1.05	1.14	-1.38	-3.65	conserved hypothetical protein [Ricinus communis]
Les.640.1.A1_at			-1.21	-1.19	-1.38	-3.86	no hits found
Les.2820.1.S1_at	AT3G29320	glucan phosphorylase, putative	-1.24	-1.65	-1.20	-3.93	RecName: Full=Alpha-1,4 glucan phosphorylase L-1 isozyme, chloroplastic/amyloplastic; AltName: Full=Starch phosphorylase L-1; Flags: Precursor
LesAffx.54132.1.S1_at	AT3G45620	transducin family protein / WD-40 repeat family protein	-1.25	-1.14	-1.23	-4.05	WD domain containing protein, putative [Solanum demissum]
Les.2923.2.S1_at	AT1G32860	glycosyl hydrolase family 17 protein	-1.82	-1.28	-1.44	-4.13	Glucan endo-1,3-beta-glucosidase precursor, putative [Ricinus communis]
Les.4356.3.S1_at	AT4G15530	PPDK (pyruvate orthophosphate dikinase); kinase/ pyruvate, phosphate dikinase	-1.80	-1.75	-1.45	-4.27	pyruvate orthophosphate dikinase [Echinochloa frumentacea]
Les.2923.1.S1_at	AT1G32860	glycosyl hydrolase family 17 protein	-1.58	-1.43	-1.41	-4.28	Glucan endo-1,3-beta-glucosidase precursor, putative [Ricinus communis]
Les.4962.1.S1_at	AT2G19580	TET2 (TETRASPANIN2)	-1.37	-1.00	-1.52	-4.72	TET2 (TETRASPANIN2) [Arabidopsis thaliana]
LesAffx.47386.1.S1_at	AT2G39570	ACT domain-containing protein	-1.91	-1.19	-1.33	-4.81	amino acid binding protein, putative [Ricinus communis]
LesAffx.69931.1.S1_at	AT5G03530	RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding	-1.70	1.27	-2.20	-4.88	RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding [Arabidopsis thaliana]
Les.3509.1.S1_at	AT4G13510	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	-1.77	1.03	-1.59	-6.52	RecName: Full=Ammonium transporter 1 member 3; AltName: Full=LeAMT1;3

LesAffx.69867.1.S1_at	AT3G16850	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	-2.24	-1.77	-1.87	-7.03	polygalacturonase-like protein [Arabidopsis thaliana]
LesAffx.1959.2.S1_at	AT1G74840	myb family transcription factor	-1.03	1.10	-1.40	-7.15	MYB transcription factor [Capsicum annuum]
LesAffx.71242.2.S1_at	AT1G68520	zinc finger (B-box type) family protein	-1.23	1.19	-1.59	-7.47	transcription factor, putative [Ricinus communis]
Les.1784.1.S1_at	AT3G05400	sugar transporter, putative	-2.16	-1.42	-1.63	-8.45	sugar transporter, putative [Arabidopsis thaliana]
Les.2254.1.A1_at			-1.63	1.97	-2.31	-8.56	no hits found
Les.1.1.S1_at	AT3G13750	BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / hemebinding / peroxidase/ sugar binding	-1.14	1.53	-1.24	-9.58	beta-galactosidase [Lycopersicon esculentum]

Cluster 4 GO:

Tomato Functional Genomics Database (http://ted.bti.cornell.edu/cgi-bin/TFGD/array/GO_analysis.cgi)

Gene Ontology term	Cluster frequency	Genome frequency of use	Raw P-value	Corrected P-value (FDR)
cellular ion homeostasis	6 out of 115 genes, 5.2%	30 out of 10209 genes, 0.3%	8.53E-07	0
cellular chemical homeostasis	6 out of 115 genes, 5.2%	30 out of 10209 genes, 0.3%	8.53E-07	0
ion homeostasis	6 out of 115 genes, 5.2%	34 out of 10209 genes, 0.3%	1.86E-06	0
myo-inositol hexakisphosphate biosynthetic process	3 out of 115 genes, 2.6%	4 out of 10209 genes, 0.0%	5.52E-06	0
singlet oxygen-mediated programmed cell death	3 out of 115 genes, 2.6%	4 out of 10209 genes, 0.0%	5.52E-06	0
circadian regulation of calcium ion oscillation	3 out of 115 genes, 2.6%	4 out of 10209 genes, 0.0%	5.52E-06	0
inositol phosphate biosynthetic process	3 out of 115 genes, 2.6%	4 out of 10209 genes, 0.0%	5.52E-06	0
myo-inositol hexakisphosphate metabolic process	3 out of 115 genes, 2.6%	4 out of 10209 genes, 0.0%	5.52E-06	0
cytosolic calcium ion homeostasis	3 out of 115 genes, 2.6%	4 out of 10209 genes, 0.0%	5.52E-06	0
cellular di-, tri-valent inorganic cation homeostasis	4 out of 115 genes, 3.5%	16 out of 10209 genes, 0.2%	2.50E-05	0.002
anthocyanin metabolic process	4 out of 115 genes, 3.5%	16 out of 10209 genes, 0.2%	2.50E-05	0.00182
di-, tri-valent inorganic cation homeostasis	4 out of 115 genes, 3.5%	16 out of 10209 genes, 0.2%	2.50E-05	0.00167
inositol biosynthetic process	3 out of 115 genes, 2.6%	6 out of 10209 genes, 0.1%	2.71E-05	0.00154
chemical homeostasis	6 out of 115 genes, 5.2%	54 out of 10209 genes, 0.5%	2.97E-05	0.00143
cellular calcium ion homeostasis	3 out of 115 genes, 2.6%	7 out of 10209 genes, 0.1%	4.71E-05	0.00133
blue light signaling pathway	3 out of 115 genes, 2.6%	7 out of 10209 genes, 0.1%	4.71E-05	0.00125
calcium ion homeostasis	3 out of 115 genes, 2.6%	7 out of 10209 genes, 0.1%	4.71E-05	0.00118
polyol biosynthetic process	3 out of 115 genes, 2.6%	8 out of 10209 genes, 0.1%	7.48E-05	0.00222
phototropism	3 out of 115 genes, 2.6%	9 out of 10209 genes, 0.1%	0.00011	0.00316
regulation of meristem growth	3 out of 115 genes, 2.6%	9 out of 10209 genes, 0.1%	0.00011	0.003
inositol phosphate metabolic process	3 out of 115 genes, 2.6%	9 out of 10209 genes, 0.1%	0.00011	0.00286
regulation of developmental growth	3 out of 115 genes, 2.6%	9 out of 10209 genes, 0.1%	0.00011	0.00273
cellular cation homeostasis	4 out of 115 genes, 3.5%	26 out of 10209 genes, 0.3%	0.00018	0.00435

cellular homeostasis	6 out of 115 genes, 5.2%	76 out of 10209 genes, 0.7%	0.0002	0.00417
cellular metal ion homeostasis	3 out of 115 genes, 2.6%	11 out of 10209 genes, 0.1%	0.00021	0.004
metal ion homeostasis	3 out of 115 genes, 2.6%	11 out of 10209 genes, 0.1%	0.00021	0.00385
cation homeostasis	4 out of 115 genes, 3.5%	30 out of 10209 genes, 0.3%	0.00033	0.00444
inositol metabolic process	3 out of 115 genes, 2.6%	13 out of 10209 genes, 0.1%	0.00036	0.005
stomatal movement	3 out of 115 genes, 2.6%	15 out of 10209 genes, 0.1%	0.00057	0.0069
response to blue light	3 out of 115 genes, 2.6%	16 out of 10209 genes, 0.2%	0.0007	0.00667
protein-chromophore linkage	3 out of 115 genes, 2.6%	16 out of 10209 genes, 0.2%	0.0007	0.00645
regulation of meristem development	3 out of 115 genes, 2.6%	17 out of 10209 genes, 0.2%	0.00084	0.01375
chromatin remodeling	3 out of 115 genes, 2.6%	19 out of 10209 genes, 0.2%	0.00118	0.01636
regulation of biological quality	10 out of 115 genes, 8.7%	284 out of 10209 genes, 2.8%	0.00134	0.02118
meristem maintenance	3 out of 115 genes, 2.6%	21 out of 10209 genes, 0.2%	0.00159	0.02457
pigment metabolic process	5 out of 115 genes, 4.3%	77 out of 10209 genes, 0.8%	0.00172	0.02389
circadian rhythm	3 out of 115 genes, 2.6%	23 out of 10209 genes, 0.2%	0.00209	0.02865
polyol metabolic process	3 out of 115 genes, 2.6%	24 out of 10209 genes, 0.2%	0.00237	0.03368
homeostatic process	6 out of 115 genes, 5.2%	122 out of 10209 genes, 1.2%	0.00251	0.03333
phagocytosis	2 out of 115 genes, 1.7%	7 out of 10209 genes, 0.1%	0.00254	0.035
positive regulation of flower development	3 out of 115 genes, 2.6%	26 out of 10209 genes, 0.3%	0.00299	0.04537
protein autoprocessing	3 out of 115 genes, 2.6%	26 out of 10209 genes, 0.3%	0.00299	0.04429
protein amino acid autophosphorylation	3 out of 115 genes, 2.6%	26 out of 10209 genes, 0.3%	0.00299	0.04326
positive regulation of post-embryonic development	3 out of 115 genes, 2.6%	26 out of 10209 genes, 0.3%	0.00299	0.04227

Supplemental Table S4. TAIR statistical regulatory element motif analysis of genes present in clusters 1, 2, 3 and 4 of the co-expression network presented in Fig. 4A. A, An over-representation analysis of particular DNA motifs in the 1 kb upstream region of the translation start site of co-expressed genes present in each of the four different clusters was performed and a maximum of 12 significantly enriched motifs is reported.

Motif	Absolute number of this motif in query (test) set	Absolute number in background (genomic set)	Number of sequences in test set containing motif	Number of sequences (out of 33602 in background) containing motif	p-value from binomial distribution	Annotation
Cluster 1						
ATTGCT;AGCAAT*	17	18778	15/78	13961	0.00002	Y-box
CCAATT:AATTGG	87	26725	59/78	17876	0.00003	CArG (MADS)
TTTGAC;GTCAAA*	118	30479	60±/78	19343	0.00017	W/TGA box
GACTTT;AAAGTC*	95	24357	54/78	16819	0.00027	
CTAAAT;ATTTAG	103	36518	63/78	21257	0.00039	
GTTGAC;GTCAAC	57	14088	39/78	10999	0.00064	W/TGA box
TTGATA;TATCAA	121	41325	66/78	23223	0.00084	
TTGACC;GGTCAA*	55	15351	40/78	11927	0.00157	W box
TTATCA;TGATAA	102	37518	63/78	22112	0.00159	
AGTCAA;TTGACT*	96	25747	52/78	17171	0.00200	
ACTATT;AATAGT	96	31032	56/78	19110	0.00246	
GGCGGC;GCCGCC	16	3529	14/78	2926	0.00433	GCC box
Cluster 2						
TCCTAC;GTAGGA*	22	8056	16/31	6967	0.00011	MYB
TGCGGC;GCCGCA*	9	2676	9/31	2472	0.00024	
TTCCTA;TAGGAA*	29	17181	22/31	13164	0.00026	AG (MADS)
TGAATC;GATTCA	46	27341	25/31	18117	0.00138	EIL (ERF1, ethylene)
TGGGGA;TCCCCA*	17	8583	15/31	7263	0.00064	
TCTTGT;ACAAGA*	17	34064	11/31	20748	0.00190	
GAATTG;CAATTC*	37	23222	23/31	16322	0.00236	
CTTCTT;AAGAAG	34	62234	16/31	25217	0.00276	
ATGGAT;ATCCAT*	39	24022	23/31	16529	0.00287	MYB
TTGGAT;ATCCAA	34	32729	26/31	20368	0.00358	MYB
GTTGGT;ACCAAC	28	18238	20/31	13588	0.00387	MYB
TTGACT;AGTCAA	28	30479	20/31	19343	0.01090	W box
Cluster 3						
GTATGG;CCATAC*	19	8171	15/26	7085	0.00004	

TCACGT;ACGTGA*	17	10218	14/26	8029	0.00072	ABRE-like
TAACGT;ACGTTA*	25	11903	15/26	9235	0.00087	ABRE-like
CATATT;AATATG	52	38354	24/26	21653	0.00108	
TACTTA;TAAGTA	25	24845	21/26	16970	0.00115	
GATTAT;ATAATC	39	32660	23/26	20466	0.00173	
ATATGT;ACATAT	55	43322	24/26	22175	0.00175	
TGTTT;ATAACA*	51	39503	24/26	22325	0.00200	
CACGTT;AACGTG*	17	9509	13/26	8009	0.00242	ABRE-like
CATACT;AGTATG	20	13369	15/26	10805	0.00440	

Cluster 4

TTCCCT;AGGAAA*	51	34894	32/36	21201	0.00044	AG (MADS)
GAGAAT;ATTCTC	37	28312	29/36	18699	0.00117	
TAAGAT;ATCTTA	51	32136	30/36	19945	0.00140	
TGATGG;CCATCA*	30	16337	22/36	12437	0.00187	SORLIP4[†]
ACCTTT;AAAGGT*	12	23122	9/36	16477	0.00193	AG (MADS)
TAATTC;GAATTA	46	29893	29/36	19201	0.00198	
TCCATC;GATGGA*	30	16521	22/36	12574	0.00218	
GCTAAT;ATTAGC*	25	14968	21/36	11804	0.00243	
TTCCCT;AGGGAA	23	14139	20/36	11102	0.00287	
TAAGAC;GTCTTA	25	14049	20/36	11219	0.00325	

* This motif was validated by POBO and there is significant enrichment of the motif in the co-expressed gene cluster.

± This set of 60 genes contain the core sequence TGAC, representing either a W box or a TGA box. See Supplemental Table S4B and Supplemental Figure S2 for further analysis of this gene set.

† This motif confers light-regulated gene expression.

B, TAIR statistical regulator element motif analysis of genes present in cluster 1 of the co-expression network presented in Fig. 4A that contain the sequence TTTGAC. An over-representation analysis of particular DNA motifs was performed in the 1000 kb upstream region of the translation start site of co-expressed genes present in cluster 1. Details on the occurrence of motifs that contain the W box consensus core motif TGACC/T are reported.

Motif	Absolute number of this motif in query (test) set	Absolute number in background (genomic set)	Number of sequences in query set containing motif	Number of sequences (out of 33602 in genomic set) containing motif	p-value from binomial distribution
TTTGAC:GTCAA	118	30479	60/60	19343/33602	4.07E-15
TTGACC:GGTCAA	51	15351	37/60	11927/33602	2.22E-05
TGACTT:AAGTCA	76	24289	44/60	16569/33602	8.76E-05
TTGACT:AGTCAA	88	25747	45/60	17171/33602	8.80 E-05
TGACCC:GGGTCA	27	6806	21/60	5934/33602	6.28 E-04

Supplemental Table S5. Metabolites showing differential accumulation in the dying seedlings (DS), as compared to the parental lines (PLS). A, Semi-polar secondary metabolites of which the relative levels are given as fold change (FC) in accumulation in the DS as compared to the PLS, at 0 hr, 1 hr, 3 hr and 5 hr after the temperature shift that induces the HR in the DS.

Compound	MSI	RT [*] (min)	Mass (D) [M-H ⁺]	Fold change				Group
				0 hr	1 hr	3 hr	5 hr	
Coumaroyldopamine (CD)	2 ^{**}	28.8	298.1086	3	2	37	116	Hydroxycinnamic acid amides (HCAAs)
Coumaroyltyramine-isoform 1 (CT1) ***	2	21.7	282.1137	19	15	20	30	
Coumaroyltyramine-isoform 2 (CT2)	1	33.4	282.1137	17	7	35	75	
Feruloyloctapan (FO)	2	30.6	328.1198	9	7	17	44	
Feruloyloctapan-hexose-isoform 1 (FO-H1)	2	22.6	490.1713	10	7	12	18	
Feruloyloctapan-hexose-isoform 2 (FO-H2)	2	23.7	490.1723	18	12	28	30	
Coumaroyltyramine-hexose (CT-H)	2	21.8	444.1662	18	15	17	27	
Feruloyltyramine-isoform 1 (FT1)	2	23.0	312.1242	16	16	17	23	
Feruloyltyramine-isoform 2 (FT2)	1	35.1	312.1242	43	14	17	19	
Feruloyltyramine-hexose-isoform 1 (FT-H1)	2	25.0	474.1770	16	15	17	21	
Feruloyltyramine-hexose-isoform 2 (FT-H2)	2	25.8	474.1773	15	16	18	24	
Salicylic acid	1	29.2	137.0245	3	2	13	26	Benzoids
Salicylate-hexose-hexose	2	9.7	461.1671	7	8	8	11	
3, 4-Dihydroxybenzoic acid ? -D-xylopyranosyl ester	2	11.7	285.0616	3	4	4	5	
Benzyl alcohol-hexose-pentose + FA [†]	2	16.1	447.1512	1	1	1	2	
Benzyl alcohol-hexose-hexose	2	13.2	431.1560	6	6	8	10	
Dehydro tomatine (S) I +FA	2	28.3	1076.5310	2	2	2	2	Alkaloids
Dehydro tomatine (S) II + FA	2	30.7	1076.5330	2	2	1	2	
Dehydro tomatine (S) II + FA	2	31.3	1076.5300	2	2	1	2	
Lycoperoside H or hydroxy tomatine I + FA	2	23.4	1094.5430	2	2	2	2	
Lycoperoside H or hydroxy tomatine III + FA	2	26.5	1094.5420	2	2	2	2	
Lycoperoside H or hydroxy tomatine III + FA	2	26.9	1094.5380	2	3	2	3	
Tomatidine + 2 hexose + 2 pentose + FA	2	33.5	1048.5370	2	2	1	2	
Tomatidine + 4 hexose + FA	2	31.9	1108.5580	2	2	2	2	
Dehydro tomatine (S) I +FA	2	28.3	1076.5310	2	2	2	2	
Dehydro tomatine (S) II + FA	2	30.7	1076.5330	2	2	1	2	
Dehydro tomatine (S) II + FA	2	31.3	1076.5320	2	2	1	2	
Alpha-tomatine	1	31.9	1078.5460	2	2	2	2	
Alpha-tomatine isomer	2	33.0	1078.5480	2	2	2	2	
Lycoperoside H or hydroxy tomatine IV + FA	2	28.0	1094.5420	2	2	2	2	
Leptinidine; Hexose , Hexose, Hexose + FA	2	27.4	944.4875	2	2	2	2	
Quercetin -hexose-hexose (3-O)	2	20.5	625.1403	2	2	2	2	
Quercetin - hexose-hexose-hexose	2	11.8	787.1945	2	2	2	2	
Quercetin 3-O-rutinoside-7-O-glucoside	2	15.4	771.1985	2	2	2	2	

Quercetin-hexose-deoxyhexose, -pentose	2	22.2	741.1882	2	2	2	2	Flavonoids
Quercetin 3-O-rutinoside	2	24.2	609.1456	2	2	1	2	
Quercetin-hexose-deoxyhexose, -hexose	2	29.8	947.2480	2	2	2	2	
Quercetin 3-O-glucoside	2	25.2	463.0877	-1	-2	-2	-1	
Kaempferol-hexose-hexose (3-O)?	2	22.9	609.1459	3	3	3	3	
Grossamide	4	47.5	623.2401	11	11	15	20	Triterpenoid glycoside
Aquilegioside H ($C_{48}H_{78}O_{20}$)	4	35.3	973.5010	38	38	37	56	
Creoside II	4	12.6	305.1614	5	7	7	10	
Sericoside ($C_{35}H_{54}O_{12}$)	4	38.3	665.3907	48	43	40	64	
Esculentoside S ($C_{42}H_{66}O_{16}$)	4	40.5	825.4269	56	55	53	79	
3-O-feruloyl quinic acid	2	20.3	367.1039	-1	-2	-2	-2	Organic acids
Caffeoyl isocitric acid + H_2O -isoform 1	2	5.8	371.0623	-1	-2	-2	-2	
Caffeoyl isocitric acid + H_2O -isoform 2	2	7.9	371.0621	-1	-2	-2	-2	
Coumaroylquinic acid	2	19.8	337.1504	1	2	1	2	
Melibionic acid	4	45.4	483.2445	-2	-2	-2	-3	
Unidentified	4	22.7	387.0957	3	4	5	5	Unknown
Unidentified	4	31.6	631.2824	3	4	6	6	
Unidentified	4	37.8	1341.6080	4	3	5	3	
Unidentified	4	31.7	1240.6050	4	3	4	3	
Unidentified	4	7.1	329.0876	4	5	7	7	
Unidentified	4	26.7	586.2446	5	4	5	7	
Unidentified	4	16.0	476.1561	5	5	6	9	
Unidentified	4	34.1	453.2350	5	5	5	7	
Unidentified	4	30.5	513.2255	6	5	5	5	
Unidentified	4	21.0	517.1568	6	6	6	8	
Unidentified	4	42.5	463.2630	6	5	7	8	
Unidentified	4	31.1	1181.5700	6	6	7	11	
Unidentified	4	24.8	637.2135	7	6	9	10	
Unidentified	4	40.4	711.3619	10	10	9	15	
Unidentified	4	41.1	857.4556	11	10	9	13	
Unidentified	4	38.9	1165.5700	12	11	13	16	
Unidentified	4	25.5	606.2198	14	10	11	14	
Unidentified	4	38.0	782.2667	14	13	13	19	
Unidentified	4	41.1	785.2931	14	13	13	20	
Unidentified	4	37.3	812.2767	20	20	23	32	
Unidentified ($C_{19}H_{36}O_{10}$) + FA	4	4.8	469.0301	-4	-3	-5	-2	
Unidentified	4	40.6	617.2621	-3	-6	-9	-6	
Unidentified ($C_{15}H_{16}O_{11}$)2	4	9.0	743.1303	-2	-4	-3	-5	
Unidentified	4	45.4	483.2445	-2	-2	-2	-3	
Unidentified ($C_{19}H_{36}O_{10}$) + FA	4	9.0	469.0293	-2	-2	-2	-3	

* Retention time.

? Position not known.

† Formic acid adduct.

**1, Identified metabolites based on authentic standards; 2, Putatively annotated compounds (e.g. without chemical reference standards, based upon physicochemical properties and/or spectral similarity with public/commercial spectral libraries); 4, Unknown compounds. Although unidentified or unclassified, these metabolites can still be differentiated and quantified based on spectral data. The reporting grades (1, 2 and 4) are assigned according to the proposed minimum reporting standards for chemical analysis (metabolomics standards initiative (MSI)) (Sumner et al., 2007).

*** Isoform 1 and isoform 2 are anticipated to refer to the cis- and trans-derivatives of the compound, respectively. Cis-derivatives are more polar than their trans-counterparts and elute earlier than their trans-derivatives. Cis-isomers are generally associated with light-induced isomerization of the natural trans isomers originally synthesized by the plant (Mühlenbeck et al., 1996).

B, Polar primary metabolites of which the relative levels are given as fold change (FC) in accumulation in the DS as compared to the PLS, at 0 hr, 1 hr, 3 hr and 5 hr after the temperature shift that induces the HR in the DS.

Compound	MSI	RT [*] (min)	RI ^{**}	Fold change				Group
				0 hr	1 hr	3 hr	5 hr	
Benzoic acid	1	14.2	1507	2	2	6	14	Benzenoids
Tyramine	1	17.0	1909	3	3	5	10	Polyamines
Putrescine	1	15.1	1730	3	3	3	6	
Dopamine	1	18.0	1909	3	3	3	6	
Tyrosine	1	17.2	1932	4	4	4	5	
Phenylalanine	1	13.9	1624	2	2	2	3	
Glutamine	1	15.5	1768	3	3	3	3	
Gamma-aminobutyric acid (GABA)	1	12.7	1525	1	1	2	2	Non protein amino acid
Trehalose	1	23.4	2705	2	7	8	27	Sugars
Xylose	2	14.2	1649	2	3	3	3	
Glucopyranose	2	18.3	2049	8	8	9	13	
Propanoic acid	1	6.3	1054	-2	-2	-2	-1	Organic acids
Phosphoenol pyruvate	1	9.3	1267	-2	-2	-2	-2	
Galactaric acid	2	17.8	1994	-2	-2	-3	-1	
Erythronic acid	2	13.0	1549	2	2	2	2	

*Retention time.

**Retention index.

† 1, Identified metabolites based on authentic standards; 2, Putatively annotated compounds (e.g. without chemical reference standards, based upon physicochemical properties and/or spectral similarity with public/commercial spectral libraries). The reporting grades (1 and 2) are assigned according to the proposed minimum reporting standards for chemical analysis (metabolomics standards initiative (MSI)) (Sumner et al., 2007).

Supplemental Table S6.

Expression of genes involved in the repression of defense signal transduction and protection against oxidative damage during mounting of the HR. The fold change in the expression of the genes in the dying seedlings (DS) relative to the parental lines (PLS) is indicated.

Probe set ID	Regulation	Fold change				Best Arabidopsis hit	Best Arabidopsis hit description
		0 hr	1 hr	3 hr	5 hr		
LesAffx.63980.1.S1_at	U_5 ¹	1	1	4	11	AT3G02800	Phosphatase/ phosphoprotein phosphatase/ protein tyrosine phosphatase
Les.4780.1.S1_at	U_5	-1	-1	2	4	AT4G33920	Protein phosphatase 2C (PP2C) family protein
LesAffx.33.1.S1_at	U_5	-1	1	2	2	AT3G62260	PP2C, putative
LesAffx.62321.1.S1_at	U_5	1	1	1	2	AT2G25070	PP2C, putative
LesAffx.344.12.S1_at	U_5	1	2	2	3	AT1G34750	PP2C, putative
Les.3869.1.S1_at	U_35	-2	2	8	7	AT1G07160	PP2C, putative
Les.31.1.S1_s_at	U_5	-2	2	1	3	AT5G03730	CTR1 (constitutive triple response 1)
LesAffx.6422.1.S1_at	U_5	1	3	2	5	AT2G26070	RTE1 (reversion to ethylene sensitivity 1)
Les.4533.1.S1_at	D_5	-1	1	-2	-2	AT5G03280	EIN2 (ethylene insensitive 2)
LesAffx.61034.1.S1_at	D_5	-1	1	-2	-3	AT1G32540	LOL1 (LSD1-like 1)
LesAffx.44417.1.S1_at	U_35	1	2	4	7	AT3G25070	RIN4 (RPM1-interacting protein 4)
LesAffx.57342.1.S1_at	D_5	-1	-1	-2	-8	AT5G17220	ATGSTF12 (glutathione S-transferase (GST) PHI 12)
LesAffx.46036.1.S1_at	U_5	1	1	1	11	AT4G02520	ATGSTF2 (GST PHI 2)
LesAffx.1959.3.S1_at	U_5	2	1	1	7	AT2G47730	ATGSTU8 (GST TAU 8)
LesAffx.24206.1.S1_at	U_5	-1	1	1	3	AT5G41210	ATGSTT1 (GST TAU 1)
Les.3735.1.S1_at	U_5	3	3	3	6	AT2G29490	ATGSTU1 (GST TAU 1)
Les.3734.1.S1_at	U_5	-1	2	2	5	AT1G78380	ATGSTU19 (GST TAU 19)
LesAffx.3002.1.S1_at	U_135	4	3	7	30	AT2G29450	ATGSTU5 (GST TAU 5)
LesAffx.55582.1.S1_at	U_5	2	1	2	11	AT2G29420	ATGSTU7 (GST TAU 7)
Les.123.1.S1_at	U_5	1	1	1	2	AT3G09270	ATGSTU8 (GST TAU 8)
Les.131.1.S1_at	U_135	1	2	4	28	AT3G09270	ATGSTU8 (GST TAU 8)
Les.4501.1.S1_at	U_5	2	2	4	6	AT3G09270	ATGSTU8 (GST TAU 8)
Les.2746.1.S1_at	U_5	2	5	5	35	AT3G09270	ATGSTU8 (GST TAU 8)

¹U_5, upregulated at t = 5 hr; U_35, upregulated at t = 3 and 5 hr; U_135, upregulated at t = 1, 3 and 5 hr; D_5, downregulated at t = 5 hr.

Supplemental Table S7. Expression of genes involved in the biosynthesis of hydroxycinnamic acid amides (HCAAs) during mounting of the HR. The fold change in the expression of the genes in the dying seedlings (DS) relative to the parental lines (PLS) is indicated.

Probe set ID	Regulation	Fold change				Best Arabidopsis hit	Gene bank best hit description
		0 hr	1 hr	3 hr	5 hr		
LesAffx.62617.1.S1_at	U_35 [†]	2	2	27	73	At5g42830	Anthranilate N-benzoyltransferase, putative [<i>Ricinus communis</i>]
Les.254.1.S1_at	U_135	2	3	6	9	At2g39030	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase (THT) 1-3 [†]
Les.4038.1.S1_at	U_35	1	2	8	26	At2g39030	THT1-3 [†]
Les.3687.1.S1_at	U_35	-1	2	4	7	At2g39030	THT7-1 [†]
Les.3686.1.S1_at	U_35	2	2	5	8	At2g39030	THT7-8 [†]

[†]U_35, upregulated at t = 3 and 5 hr; U_135, upregulated at t = 1, 3 and 5 hr.

[†] Characterized genes in *Solanum lycopersicum*.

Supplemental Table S8. Affymetrix ID, locus ID in the tomato genome sequence, gene description and nucleotide sequences of primers used for qRT-PCR gene expression analysis.

Probe set ID	Transcript locus ID	Best hit description	Forward primer	Reverse primer
Les.3662.1.S1_at	Solyc01g095080.2.1	ACS2 (1-aminocyclopropane-1-carboxylate synthase)	AATGTCAAGAGGCCAGGGTGGTTCC	TCCTCGCGAGCGCAATATCAAC
LesAffx.10955.1.S1_at	Solyc06g074530.1.1	ADT4 (arogenate dehydratase 4)	AGGAACGAGCGTGCTGTTCAAG	CGAGACTCGATCTCGTCAAGCTG
Les.129.1.S1_at	Solyc01g109140.2.1	DES (divinyl ether synthase)	CAAGTCTGCTGTGTCATGTTGG	GCTTCGCCACAAACCTGAATAG
LesAffx.16424.1.S1_s_at	Solyc06g005170.2.1	MAPK3 (mitogen-activated protein kinase 3)	GCTGCCATAGATGTTGGTCTGTG	TGTAGGAGTGCCAAGAAGCTCAG
Les.4038.1.S1_at	Solyc08g068770.1.1	THT-1-3 (N-hydroxycinnamoyl-CoA: tyamine N-hydroxycinnamoyl transferase)	GCTTCTATGACAAGCCTGGTTC	ACTGCGATTATCCCTCAACCG
LesAffx.3554.1.A1_at	Solyc02g065090.2.1	PLP4 (patatin-like protein-4)	GAGCATTGATGGAGGTGGTATCAG	TGCATTGGTCATCAAGTTCTG
LesAffx.9910.1.S1_at	Solyc03g116890.2.1	WRKY18 (transcription factor)	AAGGTTCAAAGAACGCTGGAAGAC	TTGTAACAGGGCTGCGGTATC
LesAffx.735.1.S1_at	Solyc09g014990.2.1	WRKY33 (transcription factor)	ACCCGAGGCAAAGAGATGGAAG	AGGTTCACGTACTGTTCTACTTGC
LesAffx.69808.1.S1_at	Solyc07g040710.2.1	CBP (calmodulin-binding family protein)	TGCATCAAGTATCTGGACCAAAG	TCGACTTGGAACCCCTACTGAC
LesAffx.63935.1.S1_at	Solyc04g005050.1.1	MMP (matrixin metallo family protein)	TGGGAGTCCAGGAGTTACGG	TCGGAGTCAAATTGGGTTGGC

Literature cited.

Mühlenbeck U, Kortenbusch A, Barz W (1996) Formation of hydroxycinnamoylamides and α -hydroxyacetovanillone in cell cultures of *Solanum khasianum*. *Phytochemistry* **42:** 1573-1579